

List of potentially matching sequences

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Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp P19196	INVA_YEREN Invasin [Yersinia enterocolitica]	1639	0.0
<input type="checkbox"/>	tr Q56889	Invasin [invA] [Yersinia enterocolitica]	1613	0.0
<input type="checkbox"/>	sp P11922	INVA_YERPS Invasin [Yersinia pseudotuberculosis]	726	0.0
<input type="checkbox"/>	tr Q56937	Invasin [inv] [Yersinia pestis]	721	0.0
<input type="checkbox"/>	tr Q8ZA73	Putative invasin (Hypothetical) [YP03944] [Yersinia pe...]	428	e-118
<input type="checkbox"/>	tr Q74QZ6	Putative invasin [YP3306] [Yersinia pestis]	428	e-118
<input type="checkbox"/>	tr Q6KC27	Intimin lambda [eae] [Escherichia coli]	342	2e-92
<input type="checkbox"/>	tr Q8KRK8	Intimin lambda [Escherichia coli]	340	6e-92
<input type="checkbox"/>	tr Q8VL95	Theta intimin [eae] [Escherichia coli]	336	1e-90
<input type="checkbox"/>	tr Q8VL00	Theta intimin [Escherichia coli]	335	2e-90
<input type="checkbox"/>	sp O31000	EAE_ECO11 Intimin (Attaching and effacing protein) (Ea...)	333	6e-90
<input type="checkbox"/>	tr Q6EV99	Intimin sigma [eae] [Escherichia coli]	332	2e-89
<input type="checkbox"/>	tr Q93FK0	Intimin [Citrobacter rodentium]	331	3e-89
<input type="checkbox"/>	tr Q93UI3	Intimin type gamma [eae] [Escherichia coli]	331	4e-89
<input type="checkbox"/>	tr Q842D8	Intimin [eae] [Escherichia coli]	330	5e-89
<input type="checkbox"/>	tr P77067	Beta intimin (Eae) [eaeA] [Escherichia coli]	330	5e-89
<input type="checkbox"/>	tr Q9RCH1	Intimin [eaeA] [Escherichia coli]	330	7e-89
<input type="checkbox"/>	tr Q9R8R5	Intimin [eae] [Escherichia coli]	330	7e-89
<input type="checkbox"/>	tr Q9S6R2	Intimin [eaeA] [Escherichia coli]	330	7e-89
<input type="checkbox"/>	tr Q6KC44	Intimin mu [eae] [Escherichia coli]	330	7e-89
<input type="checkbox"/>	tr Q47018	Intimin [eaeA] [Escherichia coli]	330	9e-89
<input type="checkbox"/>	tr Q8X6G3	Putative adhesin [eaeH] [Escherichia coli O157:H7]	329	1e-88
<input type="checkbox"/>	tr Q93K93	Intimin-kappa [eae-kappa] [Escherichia coli]	329	1e-88
<input type="checkbox"/>	tr Q7AHB0	Putative invasin [ECs0336] [Escherichia coli O157:H7]	329	1e-88
<input type="checkbox"/>	tr Q8FKK3	Putative adhesin [eaeH] [Escherichia coli O6]	329	1e-88
<input type="checkbox"/>	tr Q93K94	Intimin-jota [eae-jota] [Escherichia coli]	328	2e-88
<input type="checkbox"/>	tr Q9LBG6	Intimin [eae] [Escherichia coli]	328	2e-88
<input type="checkbox"/>	tr Q6KC43	Intimin nu [eae] [Escherichia coli]	328	2e-88
<input type="checkbox"/>	tr Q8KRL1	Intimin epsilon 2 [Escherichia coli]	327	4e-88
<input type="checkbox"/>	tr Q9EXN4	Intimin zeta [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/>	tr Q8KRK9	Intimin beta 2 [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/>	sp Q07591	EAE_CITFR Intimin (Attaching and effacing protein) (Ea...)	326	1e-87
<input type="checkbox"/>	tr Q6QZW1	Eae (Fragment) [Escherichia coli]	326	1e-87
<input type="checkbox"/>	tr Q6KC41	Intimin pi [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/>	tr Q6KC42	Intimin xi [eae] [Escherichia coli]	325	2e-87
<input type="checkbox"/>	tr Q8VL93	Zeta intimin [Escherichia coli]	325	2e-87

<input type="checkbox"/> tr	<u>Q846P2</u>	Intimin-zeta [eae] [Escherichia coli]	325	3e-87
<input type="checkbox"/> sp	<u>P43261</u>	EAЕ_ECO57 Intimin (Attaching and effacing protein) (Ea...	324	4e-87
<input type="checkbox"/> tr	<u>Q9RGP3</u>	Intimin type epsilon [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/> tr	<u>Q9R8B5</u>	Gamma intimin [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/> tr	<u>Q9R8B4</u>	Gamma intimin [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/> tr	<u>Q8RSS9</u>	Intimin eta [eae] [Escherichia coli]	323	1e-86
<input type="checkbox"/> tr	<u>Q84FQ2</u>	Intimin epsilon [Escherichia coli]	323	1e-86
<input type="checkbox"/> tr	<u>Q93UI4</u>	Intimin type beta [eae] [Escherichia coli]	322	2e-86
<input type="checkbox"/> tr	<u>Q8RNT8</u>	Intimine type epsilon [eae] [Escherichia coli]	322	2e-86
<input type="checkbox"/> tr	<u>Q8KRL0</u>	Intimin alpha 2 [eae] [Escherichia coli]	321	4e-86
<input type="checkbox"/> tr	<u>Q06896</u>	Intimin [eae] [Escherichia coli]	318	2e-85
<input type="checkbox"/> tr	<u>Q52620</u>	Intimin [eaeA] [Escherichia coli]	318	3e-85
<input type="checkbox"/> sp	<u>P19809</u>	EAЕ_ECO27 Intimin (Attaching and effacing protein) (Ea...	317	6e-85
<input type="checkbox"/> tr	<u>Q9F609</u>	Intimin type epsilon (Fragment) [eaeA] [Escherichia coli]	316	1e-84
<input type="checkbox"/> tr	<u>Q8KRL2</u>	Intimin iota 2 [Escherichia coli]	316	1e-84
<input type="checkbox"/> tr	<u>Q6KAV7</u>	Intimin rho [eae] [Escherichia coli]	311	2e-83
<input type="checkbox"/> tr	<u>Q7N599</u>	Similarities with putative adhesin [plu2057] [Photorha...	310	9e-83
<input type="checkbox"/> tr	<u>Q9EYM6</u>	Intimin type epsilon (Fragment) [eaeA] [Escherichia coli]	310	9e-83
<input type="checkbox"/> tr	<u>Q8XB95</u>	Putative invasin [z5932] [Escherichia coli O157:H7]	304	4e-81
<input type="checkbox"/> tr	<u>Q7A8L6</u>	Putative invasin [ECs5290] [Escherichia coli O157:H7]	298	4e-79
<input type="checkbox"/> tr	<u>Q8D083</u>	Putative adhesin [y2605] [Yersinia pestis]	296	1e-78
<input type="checkbox"/> sp	<u>P76347</u>	YEEJ_ECOLI Hypothetical protein yeeJ [yeeJ] [Escherich...	293	1e-77
<input type="checkbox"/> sp	<u>Q8X8V7</u>	YEEJ_ECO57 Hypothetical protein yeeJ [z3135] [Escheric...	289	2e-76
<input type="checkbox"/> tr	<u>Q7CQ17</u>	SinH [sinH] [Salmonella typhimurium]	245	3e-63
<input type="checkbox"/> tr	<u>Q9XC19</u>	SinH [sinH] [Salmonella typhimurium]	245	3e-63
<input type="checkbox"/> tr	<u>Q8FF61</u>	SinH homolog [c3031] [Escherichia coli O6]	235	3e-60
<input type="checkbox"/> tr	<u>Q9L574</u>	Invasin-like SivH [sivH] [Salmonella typhi]	233	9e-60
<input type="checkbox"/> tr	<u>Q7X2C2</u>	Aec1 precursor [aec1] [Escherichia coli]	233	1e-59
<input type="checkbox"/> sp	<u>P36943</u>	EAЕH_ECOLI Attaching and effacing protein homolog prec...	209	1e-52
<input type="checkbox"/> sp	<u>P39165</u>	YCHO_ECOLI Hypothetical protein ychO [ychO] [Escherich...	199	2e-49
<input type="checkbox"/> tr	<u>Q8XDD4</u>	YchP protein [ychP] [Escherichia coli O157:H7]	198	3e-49
<input type="checkbox"/> tr	<u>Q7AEU6</u>	Putative factor [ECs1725] [Escherichia coli O157:H7]	198	3e-49
<input type="checkbox"/> tr	<u>Q83RN8</u>	Putative factor [ychP] [Shigella flexneri]	198	4e-49
<input type="checkbox"/> tr	<u>Q7UCS2</u>	Putative factor [ychP] [Shigella flexneri]	198	4e-49
<input type="checkbox"/> tr	<u>Q8FHZ3</u>	Hypothetical protein ychP [ychP] [Escherichia coli O6]	195	3e-48
<input type="checkbox"/> tr	<u>Q93GR3</u>	Putative adhesin [PSLT034] [Salmonella typhimurium]	190	8e-47
<input type="checkbox"/> tr	<u>Q8ZP33</u>	Putative invasin [ychP] [Salmonella typhimurium]	186	1e-45
<input type="checkbox"/> tr	<u>Q8Z7G3</u>	Putative invasin [STY1284] [Salmonella typhi]	186	1e-45
<input type="checkbox"/> tr	<u>Q8ZP78</u>	Homology to invasin C of Yersinia; intimin [STM1669] [...	158	5e-37
<input type="checkbox"/> tr	<u>Q83T27</u>	Invasin-like protein [t1573] [Salmonella typhi]	157	1e-36
<input type="checkbox"/> tr	<u>Q8Z795</u>	Invasin-like protein [STY1395] [Salmonella typhi]	156	1e-36
<input type="checkbox"/> tr	<u>Q7WR47</u>	Putative adhesin [BB0110] [Bordetella bronchiseptica (...	85	5e-15
<input type="checkbox"/> tr	<u>Q7W286</u>	Putative adhesin [BPP0104] [Bordetella parapertussis]	85	6e-15
<input type="checkbox"/> tr	<u>Q7WAX9</u>	Putative outer membrane ligand binding protein [bipA] ...	70	1e-10
<input type="checkbox"/> tr	<u>Q9APE8</u>	Putative outer membrane ligand binding protein [bipA] ...	69	4e-10

<input type="checkbox"/>	tr Q7VZ27	Putative outer membrane ligand binding protein [bipA]	...	69	4e-10
<input type="checkbox"/>	tr Q7VR49	Putative adhesin [eaeH] [Candidatus Blochmannia florid...	...	67	1e-09
<input type="checkbox"/>	tr Q52708	Outer membrane protein A (Fragment) [ompA] [Rickettsia...	...	53	3e-05
<input type="checkbox"/>	tr Q6CD35	Similarity [YALI0C04136g] [Yarrowia lipolytica CLIB99]	...	53	3e-05
<input type="checkbox"/>	tr Q82XT8	Hemolysin-type calcium-binding region:RTX N-terminal d...	...	51	1e-04
<input type="checkbox"/>	sp Q52657	OMPA_RICCN Outer membrane protein A precursor (190 kDa...	...	50	2e-04
<input type="checkbox"/>	tr Q6CPZ4	Kluyveromyces lactis strain NRRL Y-1140 chromosome E o...	...	50	2e-04
<input type="checkbox"/>	sp Q8TFG9	YL61_SCHPO Hypothetical serine/threonine-rich protein	47	0.002
<input type="checkbox"/>	tr Q9C105	SPAPB1E7.04c protein [SPAPB1E7.04c] [Schizosaccharomy...	...	47	0.002
<input type="checkbox"/>	tr Q722C9	Cell wall surface anchor family protein [LMOf2365_0805...	...	46	0.003
<input type="checkbox"/>	tr Q76I98	Bacterial immunoglobulin [is2-2] [Leptospira interrogan...	...	46	0.003
<input type="checkbox"/>	tr Q7U7M8	Hypothetical [SYNW0953] [Synechococcus sp. (strain WH8...	...	45	0.004
<input type="checkbox"/>	tr Q8FGD9	Hypothetical protein c2439 [c2439] [Escherichia coli O6]	...	45	0.006
<input type="checkbox"/>	tr Q6KB38	Intimin zeta (Fragment) [eae] [Escherichia coli]	...	45	0.006
<input type="checkbox"/>	tr Q6AHX5	Hypothetical protein DKFZp686019206 [DKFZp686019206] [...	...	45	0.006
<input type="checkbox"/>	sp P15921	OMPA_RICRI Outer membrane protein A precursor (190 kDa...	...	45	0.007
<input type="checkbox"/>	tr Q8VVW0	Intimin-lambda (Fragment) [eae-lambda] [Escherichia coli]	...	44	0.010
<input type="checkbox"/>	tr Q8VLL9	Intimin (Fragment) [eae] [Escherichia coli]	...	44	0.010
<input type="checkbox"/>	tr Q6KBV3	Intimin zeta (Fragment) (Fragment) [eae] [Escherichia	44	0.010

Alignments

sp P19196
INVA_YEREN

Invasin [Yersinia enterocolitica]

835 AA
align

Score = 1639 bits (4243), Expect = 0.0
Identities = 819/835 (98%), Positives = 819/835 (98%)

Query: 1 MYSFFNTLTVTKXXXXXXXXXXXXXXTYGFSQQHYFNSEALENPAEHNEAFNKIISTG 60
MYSFFNTLTVTK TYGFSQQHYFNSEALENPAEHNEAFNKIISTG
Sbjct: 1 MYSFFNTLTVTKIISRLILSIGLIFGIFTYGFSQQHYFNSEALENPAEHNEAFNKIISTG 60

Query: 61 TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD 120
TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD
Sbjct: 61 TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD 120

Query: 121 SASYVFFSQLGIRNKDSRNTLNIGAVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAW 180
SASYVFFSQLGIRNKDSRNTLNIGAVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAW
Sbjct: 121 SASYVFFSQLGIRNKDSRNTLNIGAVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAW 180

Query: 181 TDYLQLSANGYFRLNGWHQSRSDFADYNERPASGGDIHVVKAYLPALPQLGGKLKYEQYRGE 240
TDYLQLSANGYFRLNGWHQSRSDFADYNERPASGGDIHVVKAYLPALPQLGGKLKYEQYRGE
Sbjct: 181 TDYLQLSANGYFRLNGWHQSRSDFADYNERPASGGDIHVVKAYLPALPQLGGKLKYEQYRGE 240

Query: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRHQETQWNLQMDYRLGESFR 300
RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRHQETQWNLQMDYRLGESFR
Sbjct: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRHQETQWNLQMDYRLGESFR 300

Query: 301 SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVALSGLPGQVSVSAQ 360
SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVALSGLPGQVSVSAQ
Sbjct: 301 SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVALSGLPGQVSVSAQ 360

Query: 361 IGSQSLQRILWNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVN 420
IGSQSLQRILWNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVN
Sbjct: 361 IGSQSLQRILWNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVN 420

Query: 421 TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS 480
TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS
Sbjct: 421 TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS 480

Query: 481 TPVAECEGVIITTSNGALPSKVTKTDAQGVISIALTSFTVGVSVTLIDIQGQQATVDVRF 540
TPVAECEGVIITTSNGALPSKVTKTDAQGVISIALTSFTVGVSVTLIDIQGQQATVDVRF
Sbjct: 481 TPVAECEGVIITTSNGALPSKVTKTDAQGVISIALTSFTVGVSVTLIDIQGQQATVDVRF 540

Query: 541 AVLPPDVNTSSFNVSPSDIVADGSMQSLTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 600
AVLPPDVNTSSFNVSPSDIVADGSMQSLTFVPRNKNNEFVSGITDLEFIQSGVPVTISP
Sbjct: 541 AVLPPDVNTSSFNVSPSDIVADGSMQSLTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 600

Query: 601 VTENADNYTASVVGNSVGDVDITPVQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
VTENADNYTASVVGNSVGDVDITPVQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK
Sbjct: 601 VTENADNYTASVVGNSVGDVDITPVQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660

Query: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAAASAPVDNQGKVNIAKTYGSTVTVTAK 720
GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAAASAPVDNQGKVNIAKTYGSTVTVTAK
Sbjct: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAAASAPVDNQGKVNIAKTYGSTVTVTAK 720

Query: 721 SKKFPSYTATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT 780
SKKFPSYTATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT

Subjct: 721 SKKFPSYTATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT 780

Query: 781 LWGEWGSLATYDSAEPGNYWTKKSTDFTMDMTTGDIPSAATAYPLCAEPQ 835

LWGEWGSLATYDSAEPGNYWTKKSTDFTMDMTTGDIPSAATAYPLCAEPQ

Subjct: 781 LWGEWGSLATYDSAEPGNYWTKKSTDFTMDMTTGDIPSAATAYPLCAEPQ 835

tr 056889 **Invasin [invA] [Yersinia enterocolitica]** 835 AA
align

Score = 1613 bits (4176), Expect = 0.0

Identities = 805/835 (96%), Positives = 811/835 (96%)

Query: 1 MYSFFNTLTVKXXXXXXXXXXXXXXTYGFSQQHYFNSEALENPAEHNEAFNKIISTG 60
MYSFFNTLTVKTYGFSQQ+YFNSEALENPAEHNEAFNKIISTG

Subjct: 1 MYSFFNTLTVKIISRLILSIGLIFGIFTYGFSQQNYFNSEALENPAEHNEAFNKIISTG 60

Query: 61 TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD 120
TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD

Subjct: 61 TSLAVSGNASNITRSMVNDAAQEVKHWLNRFGTTQVNVDKFKFSLKESSLDWLLPWYD 120

Query: 121 SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAW 180
SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNT YDNDMTGHNHRIGVGAEAW

Subjct: 121 SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTFYDNDMTGHNHRIGVGAEAW 180

Query: 181 TDYLQLSANGYFRLNGWHQSRDFADYNERPASGGDIHVKAYLPALPQLGGKLKYEQYRGE 240
TDYLQLSANGYFRLNGWHQSRDF DYNERPASGGDIHVKAYLPALPQLGGKLKYEQYRGE

Subjct: 181 TDYLQLSANGYFRLNGWHQSRDFDYNERPASGGDIHVKAYLPALPQLGGKLKYEQYRGE 240

Query: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVQDQRMGKSRQHEIQWNLQMDYRLGESFR 300
RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVQDQRMGKSRQHEIQWNLQMDYRLGESFR

Subjct: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVQDQRMGKSRQHEIQWNLQMDYRLGESFR 300

Query: 301 SQFSPAVVAGTRLLAESRYNLVERNPNVLEYQKQNTIKLAFSPAVLSPGLPGQVSVSAQ 360
SQFSPAVVAGTRLLAESRYNLVERNPNVLEYQKQNTIKLAFSPAVLSPGLPGQVSVSAQ

Subjct: 301 SQFSPAVVAGTRLLAESRYNLVERNPNVLEYQKQNTIKLAFSPAVLSPGLPGQVSVSAQ 360

Query: 361 IQSQSALQRILWNDAAQWVAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVN 420
IQSQSALQRILW+DAQW+A GGKLIPVSAT+YNNVVLPPYKPMAPASRTVGKTGESEAAVN

Subjct: 361 IQSQSALQRILWDDAQWIAVGGKLIPVSATNNVVLPPYKPMAPASRTVGKTGESEAAVN 420

Query: 421 TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS 480
TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS

Subjct: 421 TYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS 480

Query: 481 TPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVVTLDIQQQATVDVRF 540
TPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVG SVVTLIDIQQQATVDVRF

Subjct: 481 TPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVVTLDIQQQATVDVRF 540

Query: 541 AVLPPDVNTSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 600
AVLPPDVNTSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP

Subjct: 541 AVLPPDVNTSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 600

Query: 601 VTENADNYTASVVGNSVGDVDITPQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
VTENADNYTASVVGNSVGDVDITPQVGGESLDLLQKRITLYP+PKIT I VNGEQFATDK

Subjct: 601 VTENADNYTASVVGNSVGDVDITPQVGGESLDLLQKRITLYPIPKITSIAVNNGEQFATDK 660

Query: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAKYKTYGSTVTVTAK 720
 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAKYKTYGSTVTVTAK
 Sbjct: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAKYKTYGSTVTVTAK 720

Query: 721 SKKFPSTATYQFKPNLWVFSGTMSSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT 780
 SKKFPSTATYQFKPNLWVFSGTMSSLQSS+EASRNCQRTDFTALIESARASNGSRSPDGT
 Sbjct: 721 SKKFPSTATYQFKPNLWVFSGTMSSLQSSIEASRNCQRTDFTALIESARASNGSRSPDGT 780

Query: 781 LWGEWGLATYDSAEPGNYWTKKTSTDFVTMDMTGDIPTSAATAYPLCAEPQ 835
 LWGEWGLATYDSAEPGNYWTKKTSTDFVTMDMTG IPTSAATAYPLCAEPQ
 Sbjct: 781 LWGEWGLATYDSAEPGNYWTKKTSTDFVTMDMTGAIPTSAATAYPLCAEPQ 835

sp P11922 **Invasin [Yersinia pseudotuberculosis]** 985 AA
INVA_YERPS align

Score = 726 bits (1874), Expect = 0.0
 Identities = 381/695 (54%), Positives = 481/695 (68%), Gaps = 43/695 (6%)

Query: 45 NPAEHNEAFNKKIISTGTLAVSGNASNITRSMVNDAANQEVKHWLNRFGTTQVNVNFDKK 104
 N + EA NK+ISTG LA SG AS++ SMV DA NQE+K WLNRFGT QVN+NFDK
 Sbjct: 102 NKEQETEAVNKMISTGARLAASGRASDVAHSMVGDAVNQEIKQWLNRFGTAQVNVLNFDKN 161

Query: 105 FSLKESSLDWLLPWYDSASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDN 164
 FSLKESSLDWL PWYDSAS++FFSQLGIRNKDSRNTLN+G G+RT + W+YG NT YDN
 Sbjct: 162 FSLKESSLDWLAPWYDSASFLFFSQLGIRNKDSRNTLN LGVGIRTLENGWLYGLNTFYDN 221

Query: 165 DMTGHNHRIGVGAEAWTDYLQLSANGYFRLNGWHQSRRDFADYNERPASGGDIHVVKAYLPA 224
 D+TGHNHRIG+GAEAWTDYLQL+ANGYFRLNGWH SRDF+DY ERPA+GGD+ AYLPA
 Sbjct: 222 DLTGHNHRIGLGAEAWTDYLQLAANGYFRLNGWHSSRDFSDYKERPATGGDLRANAYLPA 281

Query: 225 LPQLGGKLKYEQYRGERVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVQDQRMGKSQHE 284
 LPQLGGKL YEQY GERVALFGKDNLQ NPYAVT G+ YTP+P +T+GVDQRMGKS +HE
 Sbjct: 282 LPQLGGKLMYEQYTGERVALFGKDNLQRNPYAVTAGINYTPVPLLTGVDQRMGKSSKHE 341

Query: 285 IQWNLQMDYRLGESFRSQFSPA VVAGTRLLAESRYNLVERNPNI VLEYQKQNTIKLAFSP 344
 QWNLQM+YRLGESF+SQ SP+ VAGTRLLAESRYNLV+RN NIVLEYQKQ +KL SP
 Sbjct: 342 TQWNLQMNQYRLGESFQS QLSPSAVAGTRLLAESRYNLVDRNNNIVLEYQKQQVVKLTLS 401

Query: 345 AVLSGLPGQVYVSQAQIQS QSALQRILWND AQWVAAGGKLIPVSATDYNVLPPYKPMAP 404
 A +SGLPGQVY V+AQ+Q SA++ I+W+DA+ +AAGG L P+S T +N+VLPPYK A
 Sbjct: 402 ATISGLPGQVYQVNAQVQGASAVREIVWSDAELIAAGGTLPLSTTQFNVLPPYKRTAQ 461

Query: 405 ASRTVGKTGESEAAVNTYTLSATAIDNHGNSSNPATLTIVVQQPQFVITSEVTDDGALAD 464
 SR + N Y+LSA A+D+ GN SN TL+V VQQPQ +T+ V DGA A+
 Sbjct: 462 VSRVT----DDLTANFYSL SALAVDHQGNRSNSFTLSVTVQQPQLTLAAVIGDGAPAN 516

Query: 465 GRTPITVKFTVTNIDSTPVAE QEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVS 524
 G+T ITV+FTV + + P+A QE VITT+NGALP+K+T+KTDA GV IALT+ T GV+V
 Sbjct: 517 GKTAITVEFTVADFEGKPLAGQE VVITTNNGALPNKITEKTDANGVARIALNTTDGVT 576

Query: 525 VTLDIQQQATVDVRFAVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGI 584
 VT + + +GQ+ +VD F S+ P+ I+ADG M S +T ++ + +G
 Sbjct: 577 VTAEEVEGQRQSVDTHFVKG TIAADKSTLAAVPTSI IADGLMASTITLELKDTYGD PQAGA 636

Query: 585 T---DLEFIQSGVPVTISPVTENAD-NYTASVVGNSVGDVDITPQVGGESLDLLQKRITL 640
 D GV +T++ D Y+A + +G +T +V G +
 Sbjct: 637 NVAFTTTLGNMGV-----ITDHNDGTYsapLTSTTLGVATVTVKVDGAA----- 680

Query: 641 YPVPKITYGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDN 700
 + VP +T VN F D P +++F + D +A+ T SS + PVD
 Sbjct: 681 FSVPSVT---VN---FTAD---PIPDAGRSSFTVSTPDILADGTM---SSTLSFVPVDK 727

Query: 701 QGKV----NIAYKTYGSTVTVTAKSKKFPSTYAT 730
 G +++ G V+++ +++ SYTAT
 Sbjct: 728 NGHFISGMQGLSFTQNGVPVSISPITEQPDSYAT 762

Score = 386 bits (991), Expect = e-105
 Identities = 205/376 (54%), Positives = 262/376 (69%), Gaps = 10/376 (2%)

Query: 462 LADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVG 521
 +ADG T+ + + PA T+ G + +T D G S LTS T+G
 Sbjct: 612 IADGLMASTITLELKDTYGDPOAGANVAFDTTLGNM-GVITDHND-GTYSAPLTSTTLG 668

Query: 522 VSVVTLIDIQQ---ATVDVRFALP-PDVTNSSFNVSPSDIVADGSMQSIITFVPRNKN 577
 V+ VT+ + G +V V F P PD SSF VS DI+ADG+M S L+FVP +KN
 Sbjct: 669 VATVTVKVDGAAFSVPSVTVNFTADPIPDAGRSSFTVSTPDILADGTMSSLFVPVDKN 728

Query: 578 NEFVSGITDLEFIQSGVPVTISPVTENADNYTASVVGNSVGDVDITPQVGGESLDLLQKR 637
 F+SG+ L F Q+GVPV+ISP+TE D+YTA+VVGNSVGDV ITPOV L LQK+
 Sbjct: 729 GHFISGMQGLSFTQNGVPVSISPITEQPDSYATVVGNSVGDVTITPQVDTLILSTLQKK 788

Query: 638 ITLYPVPKITYGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAP 697
 I+L+PVP +TGI VNG+ FATDKGFPKT F ATFQL M++DVANNTQY+W+SS+ +
 Sbjct: 789 ISLFPVPTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSFTPNS 848

Query: 698 VDNQGKVNIAYKTYGSTVTVTAKSKKFPSTYATYQFKPNLWVFSGTMSLQSSVEASRNCQ 757
 V++QG+V I Y+TY S V VTAKSKKFPSTY+ +Y+F PN W++ G SL SS+EASR CQ
 Sbjct: 849 VNDQGQVTITYQTY-SEVAVTAKSKKFPSTYRFYPNRWIYDGGRSLVSSLEASRQCC 907

Query: 758 RTDFTALIESARASNGSRSPDGTLWGEWGLATYDSAEWPSGNWTKKTSTDFVTMDMTT 817
 +D +A++ES+RA+NG+R+PDGTLWGEWGL Y S++W SG YW KKTSTDF TM+M T
 Sbjct: 908 GSDMSAVLESSRATNGTRAPDGTLWGEWGLTAY-SSDWQSGEYWVKTSTDFETMNMDT 966

Query: 818 GDI-PTSAATAYPLCA 832
 G + P A A+PLCA
 Sbjct: 967 GALQPGPAYLAFPLCA 982

tr Q56937 Invasin [inv] [Yersinia pestis] 987 AA
align

Score = 721 bits (1861), Expect = 0.0
 Identities = 381/696 (54%), Positives = 480/696 (68%), Gaps = 44/696 (6%)

Query: 45 NPAEHNEAFNKKISTGTLAVSGNASNITRSMVNDAAANQEVKHWLNRGTTQVNVNFDKK 104
 N + EA NK+ISTG LA SG AS++ SMV DA NQE+K WLNRGFT QVN+NFDK
 Sbjct: 103 NKEQETEAVNKMISTGARLAASGRASDVAHSMVGDAVNQEIKQWLNRGTAQVNLFNFDKN 162

Query: 105 FSLKESSLDWLLPWYDSASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDN 164

FSLKESSLDWL PWYDSAS++FFSQLGIRNKDSRNTLN+G G+RT + W+YG NT YDN
 Sbjct: 163 FSLKESSLDWLAPWYDSASFLFFSQLGIRNKDSRNTLNLngVGIRTLENGWLYGLNTFYDN 222

Query: 165 DMTGHNHRIGVGAEAWTDYLQLSANGYFRLNGWHQS RDFADYNERPASGGDIHVKAYLPA 224
 D+TGHNHRIG+GAEAWTDYLQL+ANGYFRLNGWH SRDF+DY ERPA+GGD+ AYLPA
 Sbjct: 223 DLTGHNHRIGLGAEAWTDYLQLAANGYFRLNGWHSSRDFSDYKERPATGGDLRANAYLPA 282

Query: 225 LPQLGGKLKYEQYRGERVA-LFGKDNLQSNP YAVTTGLIYTPIPFITLGVDQRMGKSRQH 283
 LPQLGGKL YEQQ GERVA LFGKDNLQ NPYAVT G+ YTP+P +T+GVDQRMGKS +H
 Sbjct: 283 LPQLGGKL MYEQYTGERVALLFGKDNLQRNP YAVTAGINYTPVPLLTGVDQRMGKSSKH 342

Query: 284 EI QWNLQMDYRLGESFRSQFSPAVVAGTRLLAESRYNLVERNP NIVLEYQKQNTIKLAFS 343
 E QWNLQMDYRLGESF+SQ SP+ VAGTRLLAESRYNLV+RN NIVLEYQKQ +KL S
 Sbjct: 343 ETQWNLQMN YRLGESFQS QLSPSAVAGTRLLAESRYNLVDRNNNIVLEYQKQQVVKLTL S 402

Query: 344 PAVL SGLPGQVY SVSAQI QSQS ALQR ILW NDAQ WVAAG GKLI PVSAT DYN VVLP PYKPMA 403
 PA +SGLPGQVY V+A Q+Q SA++ I+W+DA+ +AAGG L P+S T +N+VLPPYK A
 Sbjct: 403 PATISGLPGQVYQVNAQVQGASAVREIVWSDAELIAAGGTLPLSTTQFNLVLP PYKRTA 462

Query: 404 PASRTVGKTGESEA AVNTYTLSATAIDNHGNSSNPATLTV I VQQPQFVITSEV TDDGALA 463
 SR + N Y+LSA A+D+ GN SN TL+V VQQPQ +T+ V DGA A
 Sbjct: 463 QVSRVT----DDLTANFYSL SALAVD HQGNRSNSFTLSVTVQQPQLTL TAAVIGDGAPA 517

Query: 464 DGRTPITVKFTVTNIDSTPVAE QEGVITTSNGALPSKVTKTDAQGVISIALTSFTVGVS 523
 G+T ITV+FTV + + P+A QE VITT+NGALP+K+T+KTDA GV IALT+ T GV+
 Sbjct: 518 SGKTAITVEFTVADFE GKPLAGQEV VIT TNNGALP N KITEKDANGV ARI ALTNT DGVT 577

Query: 524 VVTLDI QGQQATV D VRFAV LPPDVTN S FN VSPSDIVADGSMQ S ILT FVPRN KNN EFVSG 583
 VVT + + + GQ+ +VD F S+ P+ I+ADG M S +T ++ + +G
 Sbjct: 578 VVTAEVEGQRQSV DTHFVKGTIAADKSTLAAVPTSIIADGLMASTITLELKDTY GDPQAG 637

Query: 584 IT--DLEFIQSGVPVTISP V TENAD-NYTASVVGNSVGDVDITPQVGGESLDL LQKRIT 639
 D GV +T++ D Y+A + ++G +T +V G +
 Sbjct: 638 ANVAFDTTLGNMGV----ITDHNDGTYSAPLTSTTLGVATVTVKVDGAA----- 682

Query: 640 LYPVPK I TGINVN G E QFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAA S A PVD 699
 + VP +T VN F D P + + +F + D +A+ T SS + PVD
 Sbjct: 683 -FSVPSVT---VN---FTAD---PIPDAGRSSFTVSTPDILADGT M---SSTLSFVPVD 728

Query: 700 NQGKV----NIA YKTYG S T V TAKSKK F P S Y T A T 730
 G + + + G V + + + + SYTAT
 Sbjct: 729 KNGHFISGMQGLSFTQNGVPVSISPI TEQ PDSY T A T 764

Score = 380 bits (975), Expect = e-104
 Identities = 201/376 (53%), Positives = 260/376 (68%), Gaps = 10/376 (2%)

Query: 462 LADGRTPI TVKFTVTNIDSTPVAE QEGVITTSNGALPSKVTKTDAQGVISIALTSFTVG 521
 +ADG T+ + + P A T+ G + +T D G S LTS T+G
 Sbjct: 614 IADGLMASTITLELKDTY GDPQAGANVA FDTTLGNM-GVITDHND--GTYSAPLTSTTLG 670

Query: 522 VSVVTL DIQGQQ---ATVDVRFAVLP-PDVTN S FN VSPSDIVADGSMQ S ILT FVPRN K N 577
 V+ VT+ + G +V V F P PD SSF VS DI+ADG+M S L+FVP +KN
 Sbjct: 671 VATVTVKVDGAAFSVPSVTVNFTADPIPDAGRSSFTVSTPDILADGT M S STLSFVPVDKN 730

Query: 578 NEFVSGITDLEFIQSGVPVTISP V TENADNYTASVVGNSVGDVDITPQVGGESLDL LQKR 637
 F+SG+ L F Q+GVPV+ISP+TE D+YTA+VVGN+ GDV ITP V L LQK+
 Sbjct: 731 GHFISGMQGLSFTQNGVPVSISPI TEQ PDSY T A T VVGNTAGDVTITPLVDTL L I STLQKK 790

Query: 638 ITLYPVPKITGINVNGEQFATDKGFPKTFNKATFQLVMNDDVANNTQYDWTSSYAAASAP 697
 I+L+PVP +TGI VNG+ FATDKGFPKT F ATFQL M++DVANNTQY+W+SS+ +
 Sbjct: 791 ISLFPVPTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVS 850

Query: 698 VDNQGKVNIAYKTYGSTVTVTAKSKKFPSTATYQFKPNLWVFSGTMSLQSSVEASRNCQ 757
 V++QG+V I Y+TY S V VTAKSKKFPST+ +Y+F PN W++G SL SS+EASR CQ
 Sbjct: 851 VNDQQGVTITYQTY-SEAVAVTAKSKKFPSTSYRFYPNRWIYDGGTSLVSSIEASRQCQ 909

Query: 758 RTDFTALIESARASNGSRSPDGTLLWGEWGLATYDSAEPNGNYWTKKTSTDFVTMDMTT 817
 +D +A++ES+RA+NG+R+PDGTLWGEWGL Y S++W SG YW K+TSTDF TM+M T
 Sbjct: 910 GSDMSAVLESSRATNGTRAPDGTLLWGEWGLTAY-SSDWQSGEYWKRTSTDFETMNMNT 968

Query: 818 GDI-PTSAATAYPLCA 832
 G + P A A+PLCA
 Sbjct: 969 GLLQPGPAYLAFPLCA 984

tr Q8ZA73 Putative invasin (Hypothetical) [YPO3944] [Yersinia pestis] 3013 AA

align

Score = 428 bits (1100), Expect = e-118
 Identities = 265/703 (37%), Positives = 382/703 (53%), Gaps = 38/703 (5%)

Query: 66 SGNASNITRSMVNDAAANQEVKHWLNRFGTTQVNVDKFKFSLKESSLWLLPWYDSASYV 125
 S ASN+ RS V + N + WLN+FGT +V +N D F L S+LD L+P DS S +
 Sbjct: 178 SDAASNMARSAVTNEINASSQQWLNQFGTARVQLNVDSDFKLDNSALDLLVPLKDSESSL 237

Query: 126 FFSQLGIRNKNDSRNTLNIGAVRFTQQSWMYGFNTSYDNDMTGHNHRIGVGAETDYLQ 185
 F+QLG+RNKDSRNT+NIGAG+R +Q WMYG NT +DND+TG N R+GVGAE TDYL+
 Sbjct: 238 LFTQLGVRNKNDSRNTVNIGAGIRQYQGDWMYGANFFDNDLTGKNRRVGVGAEVATDYLK 297

Query: 186 LSANGYFRLNGWHQSRRDFADYNERPASGGDIHVVKAYLPALPQLGGKLKYEQYRGERVALF 245
 SAN YF L GWHQSRRDF+ Y+ERPA G DI +AYLPA PQLGGKL YE+YRG+ VALF
 Sbjct: 298 FSANTYFGLTGWHQSRRDFSSYDERPADGFDIRTEAYLPAYPQLGGKLMYEKYRGDEVALF 357

Query: 246 GKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRQHEIQWNLQMDYRLGESFRSQFSP 305
 GKD+ Q +P+AVT G+ YTP+P +T+G + R GK + N+Q++YR+G+ + Q
 Sbjct: 358 GKDDRQKDPHAVTLGVNYTPVPLVTIGAEHREGKGNNNNNTSVNVQLNYRMQWPNDQIDQ 417

Query: 306 AVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVALSGLPGQVYSVSAQIQSQS 365
 + VA R LA SRY+LVERN NIVL+Y+KQ I L P +SG G +--+AQ+---+
 Sbjct: 418 SAVAANRTLAGSRYDLVERNNTVLDYKKQELIHLVL-PDRISGSGGGAITLTAQVRAKY 476

Query: 366 ALQRILWNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLS 425
 RI W+ AGG P++ + +V LP Y+ + S NT+T+S
 Sbjct: 477 GFSRIEWDATPLENAGGSTSPLTQSSLVTLPFYQHILRTS-----NTHTIS 523

Query: 426 ATAIDNHGNSSNPATLTIVQQPQFVITSE--TDDGALADGRTPITVKFTVTNIDSTPV 483
 A A D GN+SN A ++ V +P+ ++ S + T D A A+G TV+ TTV+ D P+
 Sbjct: 524 AVAYDAQGNASNRAVTSIEVTRPETMVISHLATTIDNATANGIATNTVQATVTDGDGQPI 583

Query: 484 AEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVVTLDIQQQATVDVRFAV- 542
 Q + A S +T A G S LT GVS V++ + +VD F
 Sbjct: 584 IGQLINFAVNTQATLSTTEARTGANGTASTTLTHTVSGVSRVSVTLGSSRSVDTTFVAD 643

Query: 543 -LPPDVTNSSFNVSPSDIVADGSMQSIITFVPRNKNNEFVSGITDLEFIQSGVPVTISPV 601
 ++T ++ V+ +D VA+GS +++ + V+ + + +G V V

Sbjct: 644 ESTAEITAANLTVTNTDSVANGSDTNVRAKVTDAYTNAVANQSVIFSAANGATVIDQTV 703

Query: 602 TENADNYTASVVGNSVGDVD-ITPQVGGESDLQKRITLYPVPKITGINVNGEQFATDK 660
 NA+ S + N+ V +T +GG+S Q T P V A

Sbjct: 704 ITNAEGIADSTLTNTTAGVSVVTATLGGQS---QQVDTTFKPGSTAAISLVKLADRAVAD 760

Query: 661 GFPKTTFNKATFQLVMNDDVAN-----NTQYDWTSSYAAASAP-VDNQGKVNIAY---K 709
 G ++ Q+V+ D N + Q D + AS P G +N + +

Sbjct: 761 G-----IDQNEIQVVLRDGTGNAPNVPMSIQADNGAIVVASTPNTGVDGTINATFTNLR 815

Query: 710 TYGSTVTVTAKSKKFPSYTATYQFKPNLWVFSGTMSLQSSVEA 752

S V+VT+ + + T T+ P V S ++ ++ +A

Sbjct: 816 AGESVVSVTSPALVGMTMTFSADPRTAVVSTLAAIDNNAKA 858

Score = 122 bits (305), Expect = 4e-26

Identities = 123/477 (25%), Positives = 199/477 (40%), Gaps = 28/477 (5%)

Query: 374 DAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNHG 433
 DA GG+ + SAT+ + + +V + S A + ++ T + N+

Sbjct: 2548 DANQNPVGGQQVAFSATNEVTLTESNGSISTPEGSVLLSVTSTQA-GVHPITGTLVSNNY 2606

Query: 434 NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTS 493
 + A Q + T V D+ ALADG T V+ V + VA+ T +

Sbjct: 2607 TDTFGAAIFIANKNTAQ-LSTLMVVDNNALADGVTRNQVRAHVV DSTGNSVADMATFTAN 2665

Query: 494 NGALPSKVTKKTDAQGVISIALTSFTVGVSVVT--LDIQQQQATVDVRFAVLPPDVTNSS 551
 GA SKVT TD G LT+ VGV+VVT L G TVD F P + +

Sbjct: 2666 RGAQLSKVTVLTDNNGDAVNLTNSLGVGTVVTAKLGTAGTPLTVFTAGP--LATLT 2723

Query: 552 FNVSPSDIVADGSMQSIITFVPRNKNNEFVSGITDLEFIQSGVPVTISP-VTENADNYTA 610
 + ++ AD S + + + + G +G +T + NA+

Sbjct: 2724 LVTTVNNAFADNSATNTVQATLKDVSIGNPIVGEVVAFAASNGATITATDGGVSNANGIVL 2783

Query: 611 SVVGNSVGDVDITPQVGGESDLQKRITLYPVPKITGINVNGEQFATDKGFPKTTFNKA 670
 + + N V V L + T + K + VNG F D GFP T F A

Sbjct: 2784 ATLTNGTAGVS---TVTATIETLTETTDTFIAMKNLDVTVNGTTFNGDAGFPTTGFVGA 2840

Query: 671 TFQLVMNDDVANNTQYDWTSSYAAASAPVDNQGKV--NIAYKTYGTVTAKSKKFPSYT 728
 TF++ D N+ YDW+SS A V G V N + T T+T+A K S

Sbjct: 2841 TFKVNSGGD---NSLYDWSSSAPALVSVSGDGVVTNAVFTGPTITISATPKGGGS-P 2896

Query: 729 ATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDF----TALIESARASNGSRSPDGTLWG 783
 +Y F+ N W + + + +A +C+ + T + +A +G R+ G LW

Sbjct: 2897 LSYSFRVNQWFINNNGATLNRADAITHCENVGYTMPTSTQVTNAATWMSGKRAV-GNLWS 2955

Query: 784 EWGSLATYDSAEG-PSGNYWTKKT--STDFVTMDMTTGDIPTSA---ATAYPLCAEP 834
 EWG + Y + W P+ +W ++ + + ++TG + T A + +C P

Sbjct: 2956 EWGDFSAYTAPGWVPAEFFWLSNNHDASTALAILSTGTLTTMGDFMAITHVMCTR 3012

Score = 60.1 bits (144), Expect = 2e-07

Identities = 54/203 (26%), Positives = 86/203 (41%), Gaps = 7/203 (3%)

Query: 418 AVNTYTLSATAIDNH--GNSSNPATLTVIVQQPQFVITSE--VTDDGALADGRTPITVK 472

A T+TL+ T++ GN T I + I + +T + ALADG +
 Sbjct: 1983 ATLTHTLAGTSVVTARGNRQSKDTTFIADRTTATIRASDLTITRNNALADGVATNAAR 2042

Query: 473 FTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVTL DI--Q 530
 VT+ + PV T+ NGAL + + TD+ G S T T G+S VT I
 Sbjct: 2043 VIVTDANGNPVPSMFVGYTSNDNGALLPTSGMTDSSGTFTHTTAGISKVTAIAIVTM 2102

Query: 531 GQQATVDVRFALPPDVNTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFI 590
 G T D F S V +D +A+ S ++I+ ++ + V+G+
 Sbjct: 2103 GISQTKDAVFIADRSTAHVSELIVVKNDSLANNSDRNIVQAHIKDAHGNVVTGMNVNFSA 2162

Query: 591 QSGVPVTISPVTEADNYTASVV 613
 V +T + VT N+ Y + +
 Sbjct: 2163 TENVTLTANTVTTNSQGYAENTL 2185

Score = 53.5 bits (127), Expect = 2e-05
 Identities = 62/250 (24%), Positives = 93/250 (36%), Gaps = 10/250 (4%)

Query: 373 NDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAANVNTTLSATAIDNH 432
 N Q V + PV T VV A + +G TG A T T + N
 Sbjct: 962 NSVQAVVSDSGGNP --TGATVVFSSNTATAQVTTVIGTTGVDGIATATLNTVAGTSNV 1019

Query: 433 G---NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGV 489
 ++ N T V IT +GA+ADG V V + + P+ V
 Sbjct: 1020 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAAVV 1079

Query: 490 ITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVTL DIQGQQATVDVRFALPPDVN 549
 +++NGA T T GV S LT G S V + A +D F + V
 Sbjct: 1080 FSSANGATILSSTMNTGVNGVASTLLHTVAGTSNVVATVDTVNANIDTF --VAGAVAT 1137

Query: 550 SSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP --TENADN 607
 + + VADG+ + + V + + V+G + F + I+ V T AD
 Sbjct: 1138 ITLTPVNGAVADGANSNSVQAVVSDGDPVTGAA-VVFSSANATAQITVIGTTGADG 1196

Query: 608 YTASVVGNSV 617
 + + N+V
 Sbjct: 1197 IATATLTNTV 1206

Score = 51.6 bits (122), Expect = 6e-05
 Identities = 63/269 (23%), Positives = 108/269 (39%), Gaps = 30/269 (11%)

Query: 458 DDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTS 517
 +DGA+ADG V+ V ++ V V + NG + +TDA G + + +
 Sbjct: 2226 NDGAVADGIQTNRVEARVYDVSDNLVPNSNVFSADNGGQLVQNDVQTDALGSAYTVSN 2285

Query: 518 FTVGVSVTLDIQGQQATVDVRFALPPDV --NSSFNVSPSDIVADGSMQSILTFVPRN 575
 GV+ VT+ G A+ F T F ++ + VA+G + + + +
 Sbjct: 2286 INTGVTKVTVTADGVSASTTTFIADRTATLVTDRFLITHDNAVANGVVENRVLLHLVD 2345

Query: 576 KNNEFVSGITDLEFIQSGVPVTISPVTEADNYTASVVGNSV-GDVIDTPQVGGESDL 634
 N+ VSG+ +G + S +T+ + + V+ N++ G D+T
 Sbjct: 2346 ANDNSVSGVEVNFSATNGASINASAITD-INGFAIGVLTNTLSPSDVT----- 2393

Query: 635 QKRITLYPVPKITGINVNNGEQFATDKGFPKTFNKFATFQLVMNDDVANNTQYDWTSSYAA 694
 +TL + V QF D T N AT V+ DD A D ++
 Sbjct: 2394 ---VTLVTPGGTESLTVT-PQFIAD---INTANIATGDFVIIDDGAVANSVD--ANEVR 2443

Query: 695 SAPVDNQGKVNIAYKTY----GSTVTVT 718
 + DNQG Y G+T+T +
 Sbjct: 2444 ARVTDNQGNIAAGYSVVFSSQNGATITTS 2472

Score = 48.5 bits (114), Expect = 5e-04
 Identities = 72/292 (24%), Positives = 101/292 (33%), Gaps = 39/292 (13%)

Query: 373 NDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTESEAAVNTYTLSATAIDNH 432
 N Q V + PV T VV A + +G TG A T T + N
 Sbjct: 1155 NSVQAVVSDSDGNPV--TGAAVVFSSANATAQITTVIGTTGADGIATATLTNTVAGTSNV 1212

Query: 433 G---NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQUEGV 489
 ++ N T V IT +GA+ADG V V + + + V
 Sbjct: 1213 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVQDANGNAITGAAVV 1272

Query: 490 ITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVTLIDIQGQQATVDVRFAVLPPDVTN 549
 +++NGA T T GV S LT G S V I A +D F + V
 Sbjct: 1273 FSSANGADIIAPTMNTGVNGVASTLLHTVAGTSNVVATIDTISANIDTAF--VAGAVAT 1330

Query: 550 SSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSG----- 583
 + + VADG+ + + + N ++G
 Sbjct: 1331 ITLTAPVNGAVADGADTNQVDALVEDANGNPITGAAVVFSSANGATILSSTMNTGVNGVA 1390

Query: 584 ---ITDLEFIQSGVPVTISPVTENADNYTASVVGNSVGDVDITPQVGGESLD 632
 +T S V TI VTEN D TA V G +V + +T V G D
 Sbjct: 1391 STFLHTVAGTSNVVATIGSVTENID--TAFVAG-AVATITLTAPVNGAVAD 1439

Score = 47.0 bits (110), Expect = 0.001
 Identities = 46/178 (25%), Positives = 69/178 (37%), Gaps = 5/178 (2%)

Query: 442 TVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQUEGVITTSNGALPSKV 501
 T V IT +GA+ADG V V + + P+ V +++NGA
 Sbjct: 1321 TAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAAVVFSSANGATILSS 1380

Query: 502 TKKTDAQGVISIALTSFTVGVSVTLIDIQGQQATVDVRFAVLPPDVTNSSFNVSPSDIVA 561
 T T GV S LT G S V I +D F + V + + VA
 Sbjct: 1381 TMNTGVNGVASTFLHTVAGTSNVVATIGSVTENIDTAF--VAGAVATITLTAPVNGAVA 1438

Query: 562 DGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISPV--TENADNYTASVVGNSV 617
 DG + + V + + V+G T + F + I+ V T AD + + N+V
 Sbjct: 1439 DGVNTNSVQAVVSDSDGNAVTGAT-VVFSSANATAQITTVIGTTGADGIATATLTNTV 1495

Score = 45.1 bits (105), Expect = 0.006
 Identities = 52/210 (24%), Positives = 90/210 (42%), Gaps = 15/210 (7%)

Query: 425 SATAIDNHGNSSNPATLTVI--VQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTP 482
 S T I G A +T + V Q +TS + D LA+G+ + VT+
 Sbjct: 1595 SNTVIAISGAHQGYARVTFVADVSTAQLKLTSLF--DNQLANGKAGNIAQALVTDADHNL 1652

Query: 483 VAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVV--TLDIQQQATVDVRF 540
 +A Q NGA+ + A G++ + + G++ V TLD GQ T++ F
 Sbjct: 1653 LANQSVSFALDNGAVIESQGDASSASGIVLMRFNNTLAGMTVTATLDSTGQETLETHF 1712

Query: 541 A---VLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVT 597

++T + N ++I + +Q ++T V N N V +T SG+ +T
 Sbjct: 1713 VAGKAASIEMTMTKDNNAVANNIDTN-EVQVLVTDVDGNAINGAVVNLT-----NSGMNIT 1767

Query: 598 ISPVTENAD-NYTASVVGNSVGDVDITPQV 626
 + VT +D TA++ G + I ++
 Sbjct: 1768 PNSVTTGSDGTATATLHTLAGSLPINARI 1797

Score = 43.9 bits (102), Expect = 0.013
 Identities = 34/114 (29%), Positives = 51/114 (43%), Gaps = 4/114 (3%)

Query: 456 VTDDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAQGVISIAL 515
 + DDGA+A+ V+ VT+ +A V ++ NGA + + T G S L
 Sbjct: 2427 IIIDGAVANSVDANEVRARVTDNQGNAIAGYSVVFSSQNGATIT-TSGITGVDGWASAKL 2485

Query: 516 TSFTVGVSVVTLDIQQQQATVDVRFALPPDVNSS---FNVSPSDIVADGSMQ 566
 T G S + + ATV DV+ ++ FN +P I+ADG MQ
 Sbjct: 2486 THIKAGESGILARLSRPMATVHTLMPYFIADVSTATLQLFNFNPIPIIADGVMQ 2539

Score = 43.9 bits (102), Expect = 0.013
 Identities = 59/303 (19%), Positives = 120/303 (39%), Gaps = 28/303 (9%)

Query: 424 LSATAIDNHGNSSNPATLTIVQQPQFVITSE--VTDDGALADGRTPITVKFTVTNIDST 481
 ++AT + + G+S N T + + S+ V D A+AD V VT+
 Sbjct: 1893 VTATVVS-GSSRNIDTTFIADVTTAHIAASDLMIVDDAVADNLKNEVHARVTDAKGN 1951

Query: 482 PVAEQEGVITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVVTLDIQQQQATVDVRA 541
 ++ Q + T+ NGA + V +D G+ LT G SVVT + + + D F
 Sbjct: 1952 VLSGQTVIFTSGNGAAITTVNGISDGGLTKATLTHTLAGTSVVTARVGNRVQSKDTTFI 2011

Query: 542 V--LPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVT-I 598
 + S ++ ++ +ADG + + + N V + +G +T
 Sbjct: 2012 ADRTTATIRASDLTITRNNALADGVATNAARVIVTDANGNPVPSMFVGYTSDNGALLPT 2071

Query: 599 SPVTENADNYTASVVGNSVGDVDITPQVGGESLDLLQKRITLYPVPKITG1INVNGEQFAT 658
 S +T+++ ++ + + G +T + + + + F
 Sbjct: 2072 SGMTDSSGTFSTTFHTTAGISKVTAIAVTMGISQTKDAV-----FIA 2114

Query: 659 DKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAAASAPVDNQGKVNIAKTYGSTVTVT 718
 D ++T + + +V ND +ANN+ + ++ A + +N+ + VT+T
 Sbjct: 2115 D---RSTAHVSELIVVKNDLANNSDRNIVQAHIKDAHGNVVTGMNVNFSA-TENVTLT 2169

Query: 719 AKS 721
 A +
 Sbjct: 2170 ANT 2172

Score = 39.3 bits (90), Expect = 0.31
 Identities = 34/158 (21%), Positives = 64/158 (39%), Gaps = 1/158 (0%)

Query: 459 DGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAQGVISIALSF 518
 D A+ADG ++ + + V I NGA+ T T G I+ T+
 Sbjct: 755 DRAVADGIDQNEIQVVLRDGTGNAVPNVPMSIQADNGAIVVASTPNTGVDGTINATFTNL 814

Query: 519 TVGVSVVTLDIQQQA-TVDVRFALPPDVNSSFNVSPSDIVADGSMQSILTFVPRNKN 577
 G SVV++ T+ + F+ P S+ ++ ADG+ +++ + N
 Sbjct: 815 RAGESVSVTSPALVGMTMTFSADPRTAVVSTLAAIDNNAKADGTDTNVVRRAWVVDAN 874

Query: 578 NEFVSGITDLEFIQSGVPVTISPVTEADNYTASVVGN 615
 V G++ +G + +PV + + Y + + N
 Sbjct: 875 GNSVPGVSVTFDAGNGAVLAQNPVVTDRNGYAENTLTN 912

tr Q74QZ6 Putative invasin [YP3306] [Yersinia pestis] 3108 AA
align

Score = 428 bits (1100), Expect = e-118
 Identities = 265/703 (37%), Positives = 382/703 (53%), Gaps = 38/703 (5%)

Query: 66 SGNASNITRSMVndaanQEVKHWLNRFGTTQVNvnFDKKFSLKESSLDWLLPWYDSASYV 125
 S ASN+ RS V + N + WLN+FGT +V +N D F L S+LD L+P DS S +
 Sbjct: 178 SDAASNMRSAVTNEINASSQQWLNFQGTARVQLNVDSDFKLDNSALDLLVPLKDSESSL 237

Query: 126 FFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAWTDYLQ 185
 F+QLG+RNKDSRNT+NIAG+R +Q WMYG NT +DND+TG N R+GVGAE TDYL+
 Sbjct: 238 LFTQLGVRNKDSRNTVNIGAGIRQYQGDWMYGANTFFDNDLTGKNRRVGVAEVATDYLK 297

Query: 186 LSANGYFRLNGWHQSRDFADYNERPASGGDIHVAKYLPALPQLGGKLKYEQYRGERVALF 245
 SAN YF L GWHQSRDF+ Y+ERPA G DI +AYLPA PQLGGKL YE+YRG+ VALF
 Sbjct: 298 FSANTYFGLTGWHQSRDFSSYDERPADGFDIRTEAYLPAYPQLGGKLMYEKYRGDEVALF 357

Query: 246 GKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRQHEIQWNLQMDYRLGESFRSQFSP 305
 GKD+ Q +P+AVT G+ YTP+P +T+G + R GK + N+Q++YR+G+ + Q
 Sbjct: 358 GKDDRQKDPHAVTLGVNYTPVPLVTIGAEHREGKGNNNNTSVNQVLNYRMQWPWNDQIDQ 417

Query: 306 AVVAGTRLLAESRYNLVERNPNIIVLEYQKQNTIKLAFSPAVALSGLPGQVYSVSAQIQSQS 365
 + VA R LA SRY+LVERN NIVL+Y+KQ I L P +SG G +--+AQ+---
 Sbjct: 418 SAVAANRTLAGSRYDLVERNNNIVLDYKKQELIHLVL-PDRISGSGGAIITLTAQVRAKY 476

Query: 366 ALQRILWNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLS 425
 RI W+ AGG P++ + +V LP Y+ + S NT+T+S
 Sbjct: 477 GFSRIEWATPLENAGGSTSPLTQSSLVTLPFYQHILRTS-----NTHTIS 523

Query: 426 ATAIDNHGNSSNPATLTIVVQQPQFVITSEV--TDDGALADGRTPITVKFTVTNIDSTPV 483
 A A D GN+SN A ++ V +P+ ++ S + T D A A+G TV+ TTV+ D P+
 Sbjct: 524 AVAYDAQGNASNRAVTSIEVTRPETMVISHLATTIDNATANGIATNTVQATVTDGDGQPI 583

Query: 484 AEQEGVITTSNGALPSKVTKKTDQGVISIALTSFTVGVSVVTLDIQQQATVDVRFAV- 542
 Q + A S +T A G S LT GVS V++ + +VD F
 Sbjct: 584 IGQLINFAVNTQATLSTTEARTGANGTASTLHTVSGVSRVSVTLGSSSRVDTTFVAD 643

Query: 543 -LPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISPV 601
 ++T ++ V+ +D VA+GS +++ + V+ + + +G V V
 Sbjct: 644 ESTAEITAANLTVTNTDSVANGSDTNVRAKVTDAYTNAVANQSVIFSA NGATVIDQTV 703

Query: 602 TENADNYTASVVGNSVGDVD-ITPQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
 NA+ S + N+ V +T +GG+S Q T P V A
 Sbjct: 704 ITNAEGIADSTLTNTTAGVSVVTATLGGQS---QQVDTTFKPGSTAAISLVKLADRAVAD 760

Query: 661 GFPKTTFNKATFQLVMDDVAN-----NTQYDWTSSYASAP-VDNQGKVNIAY---K 709
 G ++ Q+V+ D N + Q D + AS P G +N + +
 Sbjct: 761 G-----IDQNEIQQVVLRDGTGNAVPNVPMSIQADNGAIVVASTPNTGVDGTINATFTNLR 815

Query: 710 TYGSTVTAKSKKFPSTYTQFKPNLWVFSQGTMSLQSSVEA 752

S V+VT+ + + T T+ P V S ++ ++ +A

Sbjct: 816 AGESVSVTSPALVGMTMTMTFSADPRTAVVSTLAAIDNNAKA 858

Score = 122 bits (305), Expect = 4e-26

Identities = 123/477 (25%), Positives = 199/477 (40%), Gaps = 28/477 (5%)

Query: 374 DAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNHG 433

DA G+ + SAT+ + ++ +V + S A + ++ T + N+

Sbjct: 2643 DANQNPVGGQQVAFSATNEVLTESNGSISTPEGSVLLSVTSTQA-GVHPITGTLVSNNY 2701

Query: 434 NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTS 493

+ A Q + T V D+ ALADG T V+ V + VA+ T +

Sbjct: 2702 TDTFGAAFIANKNTAQ-LSTLMVVDNNALADGVTRNQVRAHVVVDSTGNSVADMAVTFTAN 2760

Query: 494 NGALPSKVTKKTDAGVISIALTSFTVGVSVVT--LDIQQQATVDVRFAVLPPDVTNSS 551

GA SKVT TD G LT+ VGV+VVT L G TVD F P + +

Sbjct: 2761 RGAQLSKVTVLTDNNDAVNTLTNSLVGTVVTAKLGTAGTPLTVFTAGP--LATLT 2818

Query: 552 FNVSPSDIVADGSMQSIITFVPRNKNEFVSGITDLEFIQSGVPVTISP-VTENADNYTA 610

+ ++ AD S + + ++ + G +G +T + NA+

Sbjct: 2819 LVTTVNNAFADNSATNTVQATLKDVGSGNPIVGEVVAFAASNGATITATDGGVSNANGIVL 2878

Query: 611 SVVGNSVGDVDITPQVGGESDLQKIRITLYPVPKITGINVNQGEQFATDKGFPKTTFNKA 670

+ + N V V L + T + K + VNG F D GFP T F A

Sbjct: 2879 ATLTNGTAGVS---TVTATIETLTETTDTFIAMKNLDVTVNGTTFNGDAGFPTTGFVGA 2935

Query: 671 TFQLVMDDVANNTQYDWTSSYAAASAPVDNQGKV--NIAYKTYGSTVTAKSKKFPSTY 728

TF++ D N+ YDW+SS A V G V N + T T+T+A K S

Sbjct: 2936 TFKVNSGGD---NSLYDWSSSAPALVSVSGDGVVTFNAVFPPTGTITISATPKGGGS-P 2991

Query: 729 ATYQFKPNLWVFSQGTMSLQSSVEASRNCQRTDF----TALIESARASNGSRSPDGLTLWG 783

+Y F+ N W + + +A +C+ + T + +A +G R+ G LW

Sbjct: 2992 LSYSFRVNQWFINNNGATLNRADAITHCENVGYTMPTSTQVTNAATWMSGKRAV-GNLWS 3050

Query: 784 EWGSLATYDSAEG-PSGNYWTKKT--STDFVTMDMTGDIPTSA---ATAYPLCAEP 834

EWG + Y + W P+ +W ++ + + ++TG + T A + +C P

Sbjct: 3051 EWGDFSAVTAPGVPAEFFWLSNNHDASTALAILSTGTLTTMGDFMAITHVMCTR 3107

Score = 60.1 bits (144), Expect = 2e-07

Identities = 54/203 (26%), Positives = 86/203 (41%), Gaps = 7/203 (3%)

Query: 418 AVNTYTLSATAIDNH--GNSSNPATLTVIVQQPQFVITSE---VTDDGALADGRTPITVK 472

A T+TL+ T++ GN T I + I + +T + ALADG +

Sbjct: 2078 ATLTHTLAGTSVVTARVGNRQSKDTTFIADRRTATIRASDLTITRNNALADGVATNAAR 2137

Query: 473 FTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGVISIALTSFTVGVSVVTLDI--Q 530

VT+ + PV T+ NGAL + + TD+ G S T T G+S VT I

Sbjct: 2138 VIVTDANGNPVPSMFVGYTSNDNGALLPTSGMTDSSGTFSTTFHTTAGISKVTAIAV 2197

Query: 531 GQQATVDVRFAVLPPDVTNSSFNVSPSDIVADGSMQSIITFVPRNKNEFVSGITDLEFI 590

G T D F S V +D +A+ S ++I+ ++ + V+G+

Sbjct: 2198 GISQTKDAVFIADRSTAHVSELIVVKNDLANNSDRNIVQAHIKDAHGNVVTGMNVNFSA 2257

Query: 591 QSGVPVTISPVTENADNYTASVV 613

V +T + VT N+ Y + +

Sbjct: 2258 TENVTLTANTVTTNSQGYAENTL 2280

Score = 56.6 bits (135), Expect = 2e-06

Identities = 63/250 (25%), Positives = 93/250 (37%), Gaps = 10/250 (4%)

Query: 373 NDAQWVAAGGKLIPVSATDYNVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNH 432
N Q V + PV T VV A + +G TG A T T + N

Sbjct: 1155 NSVQAVVSDSDGNPV--TGAAVFSSANATAQITTVIGTTGADGIATATLTNTVAGTSNV 1212

Query: 433 G---NSSNPATLTIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQUEGV 489
++ N T V IT +GA+ADG V V + + P+ V

Sbjct: 1213 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAADV 1272

Query: 490 ITTSNGALPSKVTKKTDAQGVISIALTSFTVGVSVVTLDIQQQATVDVRFAVLPPDVN 549
+++NGA T T GV S LT G S V + A +D F +P V

Sbjct: 1273 FSSANGATILSSTMNTGVNGVASTLLHTVAGTSNVATVDTVNANIDTAF--VPGAVAT 1330

Query: 550 SSFNVSPSDIVADGSMQSIITFVPRNKNNEFVSGITDLEFIQSGVPVTISPV--TENADN 607
+ + VADG+ + + V + V+G + F + I+ V T AD

Sbjct: 1331 ITLTTPVNGAVADGANSNSVQAVVSDSEGNNAVAGAA-VVFSSANATAQITTVIGTTGADG 1389

Query: 608 YTASVVGNSV 617

+ + N+V

Sbjct: 1390 IATATLTNTV 1399

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Swiss-Prot Release 44.5 of 13-Sep-2004

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INVA_YEREN (P19196)

Invasin. *Yersinia enterocolitica*

INVA_YERPS (P11922)

Invasin. - *Yersinia pseudotuberculosis*

IPAA_SHIFL (P18010)

Invasin ipaA (70 kDa antigen). {GENE: Name=ipaA; OrderedLocusNames=CP0125} - *Shigella flexneri*

IPAB_SHIDY (Q03945)

Invasin ipaB (62 kDa antigen). {GENE: Name=ipaB} - *Shigella dysenteriae*

IPAB_SHIFL (P18011)

Invasin ipaB (62 kDa antigen). {GENE: Name=ipaB; OrderedLocusNames=CP0128} - *Shigella flexneri*

IPAC_SHIDY (Q03946)

Invasin ipaC (42 kDa antigen). {GENE: Name=ipaC} - *Shigella dysenteriae*

IPAC_SHIFL (P18012)

Invasin ipaC (42 kDa antigen). {GENE: Name=ipaC; OrderedLocusNames=CP0127} - *Shigella flexneri*

IPAD_SHIDY (Q03947)

Invasin ipaD (37 kDa membrane antigen). {GENE: Name=ipaD} - *Shigella dysenteriae*

IPAD_SHIFL (P18013)

Invasin ipaD (36 kDa membrane antigen). {GENE: Name=ipaD; OrderedLocusNames=CP0126} - *Shigella flexneri*

YADA_YEREN (P31489)

Invasin precursor (Outer membrane adhesin). {GENE: Name=yadA; Synonyms=yopA, invA, yop1} - *Yersinia enterocolitica*

YADA_YERPS (P10858)

Invasin precursor (Outer membrane adhesin). {GENE: Name=yadA; Synonyms=yopA, invA, yop1} - *Yersinia pseudotuberculosis*

Search in TrEMBL: There are matches to 45 out of 1400820 entries

Q07390

Invasin 1 {GENE:Name=inv1} - *Mycobacterium avium*

Q07391

Invasin 2 {GENE:Name=inv2} - *Mycobacterium avium*

Q84129

Predicted polysaccharide hydrolase-invasin repeat family {GENE:Name=ydhO; OrderedLocusNames=CT127} - *Chlamydia trachomatis*

Q84606

Invasin repeat family phosphatase {GENE:Name=papQ; OrderedLocusNames=CT601} - *Chlamydia trachomatis*

Q84764

Muramidase (Invasin repeat family) {GENE:Name=nlpD; OrderedLocusNames=CT759} - *Chlamydia trachomatis*

Q47380

Invasin - *Escherichia coli*

Q56889

Invasin {GENE:Name=invA} - *Yersinia enterocolitica*

Q56937

Invasin {GENE:Name=inv} - *Yersinia pestis*

Q6T8F2

Putative invasin-like protein (Fragment) - *Chlamydia suis*

Q6T8F6

TetR(C)-invasin fusion protein (Fragment) - *Chlamydia suis*

Q6T8F7

Invasin-like protein (Fragment) - *Chlamydia suis*

Q6T8G9

Invasin-like protein (Fragment) - *Chlamydia suis*

Q74QZ6

Putative invasin {GENE:OrderedLocusNames=YP3306} - *Yersinia pestis*

Q7A8L6

Putative invasin {GENE:OrderedLocusNames=ECs5290} - *Escherichia coli* O157:H7

Q7AGX0

Adhesin/invasin-like protein {GENE:OrderedLocusNames=ECs0548} - *Escherichia coli* O157:H7

Q7AHB0

Putative invasin {GENE:OrderedLocusNames=ECs0336} - *Escherichia coli* O157:H7

Q7N592

Similar to putative invasin and adhesin {GENE:OrderedLocusNames=plu2064} - *Photorhabdus luminescens* (subsp. *laumondii*)

Q83T27

Invasin-like protein {GENE:OrderedLocusNames=t1573} - *Salmonella typhi*

Q8EFM1

Invasin domain protein {GENE:OrderedLocusNames=SO1949} - *Shewanella oneidensis*

Q8FY77

Intimin/invasin family protein {GENE:OrderedLocusNames=BR2009} - *Brucella suis*
Q8KH85 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KHF7 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KHP5 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KI42 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KUJ1 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KUJ6 Putative adhesin/invasin - *Neisseria meningitidis*

Q8KWG5 Putative invasin protein {GENE:Name=agg3B} - *Escherichia coli* [Plasmid pAA-like]

Q8RBD9 Soluble lytic murein transglycosylase and related regulatory proteins (Some contain LysM/invasin domains) {GENE:Name=MltE2; OrderedLocusNames=TTE0883} - *Thermoanaerobacter tengcongensis*

Q8RBE4 Soluble lytic murein transglycosylase and related regulatory proteins (Some contain LysM/invasin domains) {GENE:Name=MltE; OrderedLocusNames=TTE0876} - *Thermoanaerobacter tengcongensis*

Q8RQ63 Putative adhesin/invasin {GENE:Name=Aa32-1-2} - *Actinobacillus actinomycetemcomitans* (*Haemophilus actinomycetemcomitans*)

Q8VM53 Putative invasin {GENE:Name=pagN} - *Salmonella enterica* IIIb 50:k:z

Q8XB95 Putative invasin {GENE:OrderedLocusNames=z5932} - *Escherichia coli* O157:H7

Q8Z795 Invasin-like protein {GENE:OrderedLocusNames=STY1395} - *Salmonella typhi*

Q8Z7G3 Putative invasin {GENE:OrderedLocusNames=STY1284, t1677} - *Salmonella typhi*

Q8ZA73 Putative invasin (Hypothetical) {GENE:OrderedLocusNames=YP03944, y3884} - *Yersinia pestis*

Q8ZP33 Putative invasin {GENE:Name=ychP; OrderedLocusNames=STM1768} - *Salmonella typhimurium*

Q8ZP78 Homology to invasin C of *Yersinia*; intimin {GENE:OrderedLocusNames=STM1669} - *Salmonella typhimurium*

Q9AM40 Invasin (Fragment) {GENE:Name=inv} - *Yersinia pseudotuberculosis*

Q9JSH2 Polysaccharide hydrolase-invasin repeat family {GENE:Name=ydhO} - *Chlamydia pneumoniae* (*Chlamydophila pneumoniae*)

Q9JXK7 Adhesin/invasin, putative {GENE:OrderedLocusNames=NMB1994} - *Neisseria meningitidis* (serogroup B)

Q9KK70

Putative invasin 996A009 (Fragment) - *Mycobacterium avium*
Q9L574

Invasin-like SivH {GENE:Name=sivH} - *Salmonella typhi*
Q9X4L4

Invasin homolog AafB {GENE:Name=aafB} - *Escherichia coli*
Q9Z704

Muramidase (Invasin repeat family) (Hypothetical protein CP0964) (Cell wall hydrolase)
{GENE:Name=nlpD; Synonyms=lytE; OrderedLocusNames=CP0964, CPn0902, CpB0934} -
Chlamydia pneumoniae (*Chlamydophila pneumoniae*)
Q9Z8T9

Polysaccharide Hydrolase-Invasin Repeat Family (NLP/P60 family protein) (P60)
{GENE:Name=ydhO; OrderedLocusNames=CP0517, CPn0245, CpB0252} - *Chlamydia*
pneumoniae (*Chlamydophila pneumoniae*)

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gene name, organism

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 Entered in TrEMBL in Release 01, November 1996
 Sequence was last modified in Release 01, November 1996
 Annotations were last modified in Release 26, March 2004

Name and origin of the protein

Protein name **Invasin**
 Synonyms None
 Gene name **Name: invA**
 From [Yersinia enterocolitica](#) [TaxID: 630]
 Taxonomy [Bacteria](#); [Proteobacteria](#); [Gammaproteobacteria](#); [Enterobacteriales](#); [Enterobacteriaceae](#); [Yersinia](#).

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=W1024;
 MEDLINE=94195100;PubMed=7511772 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Pepe J.C., Badger J.L., Miller V.L.;
 "Growth phase and low pH affect the thermal regulation of the *Yersinia enterocolitica* inv gene."; Mol. Microbiol. 11:123-135(1994).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=W1024;
 MEDLINE=98048470;PubMed=9387224 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Fauconnier A., Allaoui A., Campos A., Van Elsen A., Cornelis G.R., Bollen A.;
 "Flagellar flhA, flhB and flhE genes, organized in an operon, cluster upstream from the inv locus in *Yersinia enterocolitica*"; Microbiology 143:3461-3471(1997).

Comments

None

Cross-references

EMBL Z48169; CAA88188.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
 PIR S54216; S54216.
 HSSP P11922; 1CWV. [HSSP ENTRY / PDB]
GO:0007155; Biological process: cell adhesion (*inferred from electronic annotation*).
 GO [QuickGo view](#)
IPR003344; Big_1.
 InterPro [IPR003535](#); Intimin.
[IPR008964](#); Invasin_intimin.
[Graphical view of domain structure](#).
 Pfam [PF02369](#); Big_1; 1.
[Pfam graphical view of domain structure](#).
 PRINTS [PR01369](#); INTIMIN.
 ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
 HOBACGEN [\[Family / Alignment / Tree\]](#)
 ProtoMap [Q56889](#).
 PRESAGE [Q56889](#).
 ModBase [Q56889](#).
 SMR [Q56889](#); C817F6D7766184E3.
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features

None

Sequence information

Length: 835 Molecular weight: 91367 CRC64: C817F6D7766184E3 [This is a checksum on the sequence]

AA	Da	10	20	30	40	50	60
MYSFFNTLTV		TKIISRLILS	IGLIFGIFTY	GFSQQNYFNS	EALENPAEHN	EAFNKKIISTG	
AA	Da	70	80	90	100	110	120
TSLAVSGNAS		NITRSMVNDA	ANQEVKHWLN	RFGTTQVNVN	FDKKFSLKES	SLDWLLPWYD	
AA	Da	130	140	150	160	170	180
SASYVFFSQL		GIRNKDSRNT	LNIGAGVRTF	QQSWMYGFNT	FYDNDMTGHN	HRIGVGAEAW	
AA	Da	190	200	210	220	230	240
TDYLQLSANG		YFRLNGWHQS	RDFVDYNERP	ASGGDIHVKA	YLPALPQLGG	KLKYEQYRGE	
AA	Da	250	260	270	280	290	300
RVALFGKDNL		QSNPYAVTTG	LIYTPIPPFIT	LGVDQRMGKS	RQHEIQWNLQ	MDYRLGESFR	

310	320	330	340	350	360
SQFSPAVVAG	TRLLAESRYN	LVERNPNVIL	EYQKQNTIKL	AFSPAVLSQL	PGQVYSVSAQ
370	380	390	400	410	420
IQSQSALQRI	LWDDAQWIAV	GGKLIPVSAT	NYNVVLPPYK	PMAPASRTVG	KTGESEAAVN
430	440	450	460	470	480
TYTLSATAID	NHGNNSNPAT	LTVIVQQPQF	VITSEVTDDG	ALADGRTPIT	VKFTVTNIDG
490	500	510	520	530	540
TPVAEQEGVI	TTSNGALPSK	VTKKTDAQGV	ISIALTSFTV	GGSVVTLDIQ	GQQATVDVRF
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AVLPPDVNTS	SFNVSPSDIV	ADGSMQSI LT	FVPRNKNNEF	VSGITDLEFI	QSGVPVTISP
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VTEENADNYTA	SVVGNSVGDV	DITPQVGGES	LDLLQKRITL	YPIPKITSIA	VNGEQFATDK
670	680	690	700	710	720
GFPKTTFNKA	TFQLVMNDDV	ANNTQYDWTS	SYAASAPVDN	QGKVNIAYKT	YGSTVTVTAK
730	740	750	760	770	780
SKKFPSYTAT	YQFKPNLWVF	SGTMSLQSSI	EASRNCQRTD	FTALIESARA	SNGSRSPDGT
790	800	810	820	830	
LWGEW GSLAT	YDSAEP PSGN	YWT KKT STDF	VTMDMTTGAI	PTSAATAYPL	CAEPQ

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[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



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Entry information

Entry name **YADA_YEREN**
 Primary accession number **P31489**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 26, July 1993
 Sequence was last modified in Release 26, July 1993
 Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **Invasin [Precursor]**
 Synonym **Outer membrane adhesin**
 Gene name **Name: yadA**
 Synonyms: yopA, invA, yop1
 From **Yersinia enterocolitica [TaxID: 630]**
 Encoded on **Plasmid pYV.**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=6471/76 / Serotype O:3;
 MEDLINE=95020586;PubMed=7934875 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
 Tamm A., Tarkkanen A., Korhonen T.K., Kuusela P., Toivanen P., Skurnik M.;
 "Hydrophobic domains affect the collagen-binding specificity and surface polymerization as well as the virulence potential of the YadA protein of *Yersinia enterocolitica*."; Mol. Microbiol. 10:995-1011(1993).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins. This protein is an adhesin forming a fibrillar matrix on the cell surface.
- **SUBCELLULAR LOCATION:** Outer membrane.

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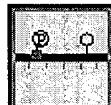
Cross-references

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PIR	S04912; S04912.
	IPR008126 ; Adhesion.
	IPR008640 ; Hep_Hag.
InterPro	IPR008635 ; HIM.
	IPR005594 ; YadA_C.
	Graphical view of domain structure .
	PF05658 ; Hep_Hag; 4.
Pfam	PF05662 ; HIM; 1.
	PF03895 ; YadA; 1.
	Pfam graphical view of domain structure .
PRINTS	PR01756 ; OMADHESIN.
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HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P31489 .
ProtoNet	P31489 .
ProtoMap	P31489 .
PRESAGE	P31489 .
DIP	P31489 .
ModBase	P31489 .
SMR	P31489 ; AC12EF68C657DAC0.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords

Outer membrane; **Plasmid**; **Signal**; **Virulence**.

Features



Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	25	25	
CHAIN	26	455	430	Invasin.

Sequence information

Length: **455 AA** [This is the length of the unprocessed precursor] Molecular weight: **47136 Da** [This is the MW of the unprocessed precursor] CRC64: **AC12EF68C657DAC0** [This is a checksum on the sequence]

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70	80	90	100	110	120

GGLNASAKGI	HSIAIGATAE	AAKGAAVAVG	AGSIATGVNS	VAIGPLSKAL	GDSAVTYGAA
130	140	150	160	170	180
STAQKDGVAI	GARASTSDTG	VAVGFNSKAD	AKNSVAIGHS	SHVAANHGYS	IAIGDRSKTD
190	200	210	220	230	240
RENSVSIGHE	SLNRQLTHLA	AGTKD TD A V N	VAQLKKEIEK	TQENTNKRSA	ELLANANAYA
250	260	270	280	290	300
DNKSSSVLGI	ANNYTD SKSA	ETLENARKEA	FAQSKDV L NM	AKAHSNSVAR	TTLETAEEHA
310	320	330	340	350	360
NSVARTTLET	AEEHANKKSA	EALASANVYA	DSKSSHTLKT	ANSYTDVTVS	NSTKKAIRES
370	380	390	400	410	420
NQYTDHKFRQ	LDNRLDKLDT	RVDKG LASSA	ALNSLFQPYG	VGKVNFTAGV	GGYRSSQALA
430	440	450			
IGSGYRVNEN	VALKAGVAYA	GSSDVMYNAS	FNIEW		

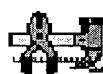
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Entry information

Entry name	YADA_YERPS
Primary accession number	P10858
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 11, July 1989
Sequence was last modified in	Release 11, July 1989
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	Invasin [Precursor]
Synonym	Outer membrane adhesin
Gene name	Name: yadA
	Synonyms: yopA, invA, yop1
From	<u>Yersinia pseudotuberculosis</u> [TaxID: <u>633</u>]
Encoded on	Plasmid pIB1.
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=YPIII;
 DOI=[10.1038/334522a0](#); MEDLINE=[88302441](#); PubMed=[3043229](#) [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Rosqvist R.](#), [Skurnik M.](#), [Wolf-Watz H.](#);
 "Increased virulence of [Yersinia pseudotuberculosis](#) by two independent mutations.";
 Nature 334:522-525(1988).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=YPIII;
 MEDLINE=[89343638](#); PubMed=[2761389](#) [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Skurnik M.](#), [Wolf-Watz H.](#);
 "Analysis of the yopA gene encoding the Yop1 virulence determinants of [Yersinia](#) spp.";
 Mol. Microbiol. 3:517-529(1989).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins. This protein is an adhesin forming a fibrillar matrix on the cell surface.
- **SUBCELLULAR LOCATION:** Outer membrane.

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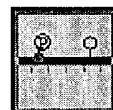
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Cross-references

EMBL	X13883; CAA32088.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S04534; S04534.
	IPR008126 ; Adhesion.
	IPR008640 ; Hep_Hag.
InterPro	IPR008635 ; HIM.
	IPR005594 ; YadA_C.
	Graphical view of domain structure .
	PF05658 ; Hep_Hag; 4.
	PF05662 ; HIM; 1.
Pfam	PF03895 ; YadA; 1.
	Pfam graphical view of domain structure .
PRINTS	PR01756 ; OMADHESIN.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P10858 .
ProtoNet	P10858 .
ProtoMap	P10858 .
PRESAGE	P10858 .
DIP	P10858 .
ModBase	P10858 .
SMR	P10858 ; EE2C55FB12B183D4.
SWISS-2DPAGE	Get region on 2D PAGE .
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords

Outer membrane; **Plasmid**; **Signal**; **Virulence**.

Features

Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	25	25	
CHAIN	26	434	409	Invasin.

Sequence information

Length: **434** AA [This is the length of the unprocessed sequence] Molecular weight: **45054** Da [This is the MW of the protein] CRC64: **EE2C55FB12B183D4** [This is a checksum on the sequence]

precursor] unprocessed precursor]

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130	140	150	160	170	180
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190	200	210	220	230	240
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370	380	390	400	410	420
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430					
SSNVMYNASF	NIEW				

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NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25:3389-3402(1997).

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Date run: 2004-09-14 18:42:59 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,568,464 sequences; 501,960,298 total letters

Taxonomic view	NiceBlast view	Printable view
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Include query sequence

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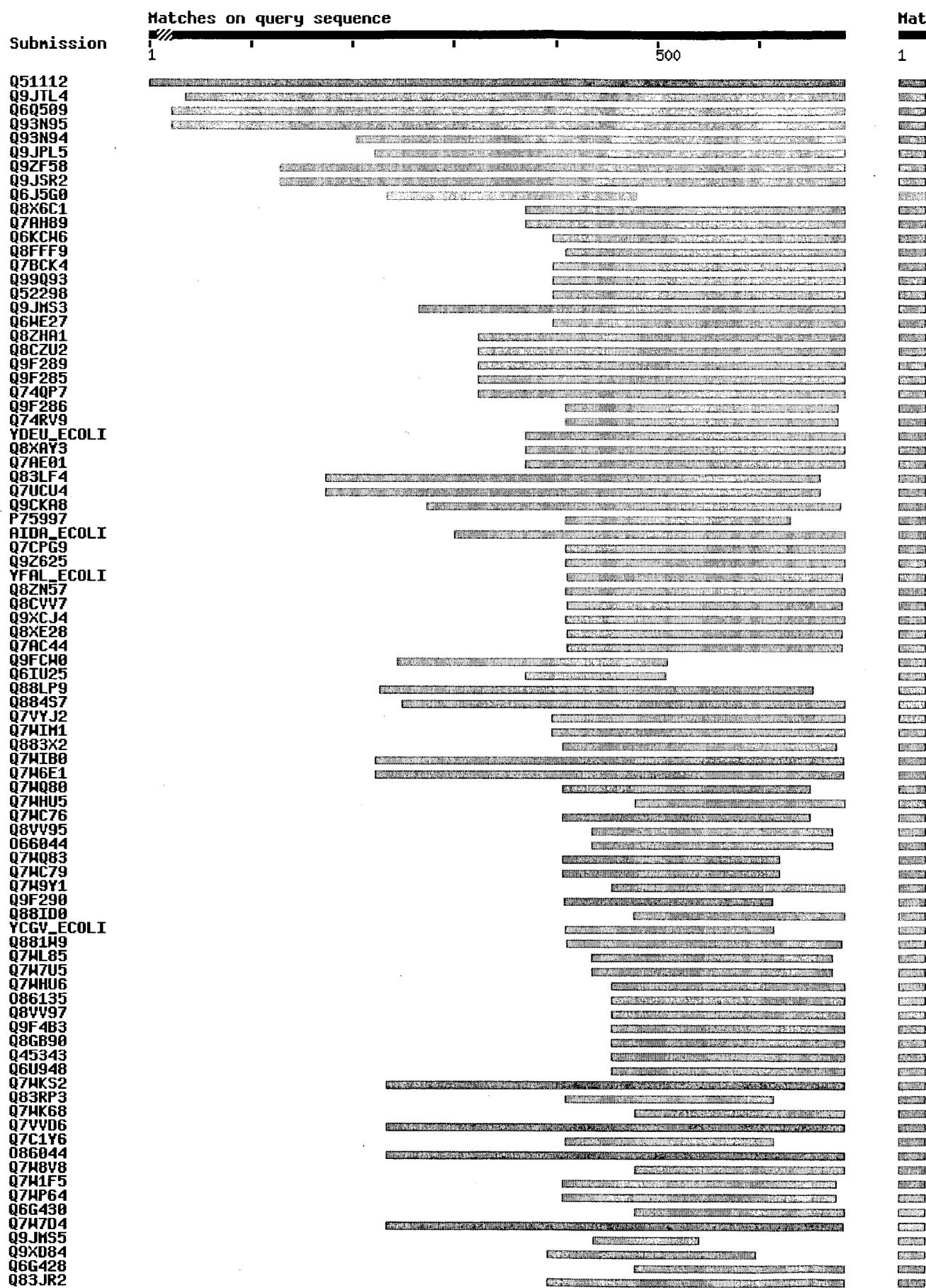
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<input type="checkbox"/>	tr Q9F289	YapD protein [yapD]	[Yersinia pestis]	130	1e-28	
<input type="checkbox"/>	tr Q9F285	YapH protein [yapH]	[Yersinia pestis]	130	1e-28	
<input type="checkbox"/>	tr Q74QP7	Putative autotransporter protein [yapH]	[Yersinia pestis]	130	1e-28	
<input type="checkbox"/>	tr Q9F286	YapG protein (Putative ATP-binding transport component...)		129	2e-28	
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<input type="checkbox"/>	tr Q8ZN57	Similar to the C-terminal region of AIDA [shdA]	[Salmo...	96	3e-18	
<input type="checkbox"/>	tr Q8CVV7	Hypothetical protein yfaL [yfaL]	[Escherichia coli O6]	96	3e-18	
<input type="checkbox"/>	tr Q9XCJ4	ShdA [shdA]	[Salmonella typhimurium]	96	3e-18	
<input type="checkbox"/>	tr Q8XE28	Putative ATP-binding component of a transport system [...]		93	1e-17	
<input type="checkbox"/>	tr Q7AC44	Putative ATP-binding component of a transport system [...]		93	1e-17	
<input type="checkbox"/>	tr Q9FCW0	Hypothetical protein [Kluyvera ascorbata]		74	9e-12	
<input type="checkbox"/>	tr Q6IU25	YdeU (Fragment)	[Escherichia coli B]	70	1e-10	
<input type="checkbox"/>	tr Q88LP9	Outer membrane autotransporter [PP1880]	[Pseudomonas p...]	66	2e-09	
<input type="checkbox"/>	tr Q884S7	Autotransporter, putative	[PSPTO2011]	[Pseudomonas syr...]	66	2e-09
<input type="checkbox"/>	tr Q7VYJ2	Autotransporter [BP1344]	[Bordetella pertussis]	65	3e-09	
<input type="checkbox"/>	tr Q7WIM1	Putative autotransporter [BB2830]	[Bordetella bronchis...	64	7e-09	
<input type="checkbox"/>	tr Q883X2	Autotransporter, putative	[PSPTO2225]	[Pseudomonas syr...]	64	9e-09
<input type="checkbox"/>	tr Q7WIB0	Putative autotransporter [BB2941]	[Bordetella bronchis...	55	3e-06	
<input type="checkbox"/>	tr Q7W6E1	Putative autotransporter [BPP2975]	[Bordetella paraper...	55	3e-06	
<input type="checkbox"/>	tr Q7WQ80	Autotransporter [BB0452]	[Bordetella bronchiseptica (A...]	54	1e-05	
<input type="checkbox"/>	tr Q7WHU5	Autotransporter [BB3111]	[Bordetella bronchiseptica (A...]	54	1e-05	
<input type="checkbox"/>	tr Q7WC76	Autotransporter [BPP0452]	[Bordetella parapertussis]	54	1e-05	
<input type="checkbox"/>	tr Q8VV95	Vag8 protein (Autotransporter) [vag8-2]	[Bordetella pe...]	52	4e-05	
<input type="checkbox"/>	tr Q66044	Vag8 [vag-8]	[Bordetella pertussis]	52	4e-05	

<input type="checkbox"/> tr	<u>Q7WQ83</u>	Autotransporter [BB0450] [Bordetella bronchiseptica (A...]	52	5e-05
<input type="checkbox"/> tr	<u>Q7WC79</u>	Autotransporter [BPP0449] [Bordetella parapertussis]	52	5e-05
<input type="checkbox"/> tr	<u>Q7W9Y1</u>	Autotransporter [BPP1618] [Bordetella parapertussis]	52	5e-05
<input type="checkbox"/> tr	<u>Q9F290</u>	YapC protein (Putative autotransporter) (Putative autot...)	51	6e-05
<input type="checkbox"/> tr	<u>Q881D0</u>	Outer membrane autotransporter [PP3069] [Pseudomonas p...	51	8e-05
<input type="checkbox"/> sp	<u>P76017</u>	YCGV_ECOLI Hypothetical protein ycgV [ycgV] [Escherich...	50	1e-04
<input type="checkbox"/> tr	<u>Q881W9</u>	Autotransporter, putative [PSPTO2763] [Pseudomonas syr...	50	2e-04
<input type="checkbox"/> tr	<u>Q7WL85</u>	Autotransporter [vag8] [Bordetella bronchiseptica (Alc...]	50	2e-04
<input type="checkbox"/> tr	<u>Q7W7U5</u>	Autotransporter [vag8] [Bordetella parapertussis]	50	2e-04
<input type="checkbox"/> tr	<u>Q7WHU6</u>	Autotransporter [BB3110] [Bordetella bronchiseptica (A...]	49	2e-04
<input type="checkbox"/> tr	<u>086135</u>	Tracheal colonization factor precursor [tcfA2] [Bordet...	49	2e-04
<input type="checkbox"/> tr	<u>Q8VV97</u>	Tcf protein [tcfA3] [Bordetella pertussis]	49	2e-04
<input type="checkbox"/> tr	<u>Q9F4B3</u>	BapB protein [bapB] [Bordetella pertussis]	49	2e-04
<input type="checkbox"/> tr	<u>Q8GB90</u>	Tracheal colonization factor [tcfA] [Bordetella pertus...	49	2e-04
<input type="checkbox"/> tr	<u>Q45343</u>	Tracheal colonization factor [tcfA] [Bordetella pertus...	49	2e-04
<input type="checkbox"/> tr	<u>Q6U948</u>	Tracheal colonization factor protein [tcfA] [Bordetell...	49	2e-04
<input type="checkbox"/> tr	<u>Q7WKS2</u>	Putative autotransporter [bapC] [Bordetella bronchisep...	48	5e-04
<input type="checkbox"/> tr	<u>Q83RP3</u>	Putative adhesion and penetration protein [SF1205] [Sh...	47	0.001
<input type="checkbox"/> tr	<u>Q7WK68</u>	Autotransporter [BB2270] [Bordetella bronchiseptica (A...]	47	0.001
<input type="checkbox"/> tr	<u>Q7VVD6</u>	Autotransporter (Pseudogene) [bapC] [Bordetella pertus...	47	0.001
<input type="checkbox"/> tr	<u>Q7C1Y6</u>	Putative adhesion and penetration protein [S1289] [Shi...	47	0.001
<input type="checkbox"/> tr	<u>086044</u>	Putative autotransporter (BapC protein) [bapC] [Bordet...	47	0.001
<input type="checkbox"/> tr	<u>Q7W8V8</u>	Autotransporter [BPP2022] [Bordetella parapertussis]	47	0.001
<input type="checkbox"/> tr	<u>Q7W1F5</u>	Autotransporter [BPP0735] [Bordetella parapertussis]	46	0.002
<input type="checkbox"/> tr	<u>Q7WP64</u>	Autotransporter [BB0821] [Bordetella bronchiseptica (A...]	45	0.003
<input type="checkbox"/> tr	<u>Q6G430</u>	Hypothetical protein [BH05490] [Bartonella henselae (R...	44	0.008
<input type="checkbox"/> tr	<u>Q7W7D4</u>	Putative autotransporter [bapC] [Bordetella parapertus...	44	0.008
<input type="checkbox"/> tr	<u>Q9JMS5</u>	YcbB protein [ycbB] [Escherichia coli]	44	0.013
<input type="checkbox"/> tr	<u>Q9XD84</u>	TibA [tibA] [Escherichia coli]	43	0.017
<input type="checkbox"/> tr	<u>Q6G428</u>	Hypothetical protein [BH05510] [Bartonella henselae (R...	42	0.029
<input type="checkbox"/> tr	<u>Q83JR2</u>	Exported serine protease SigA [sigA] [Shigella flexneri]	42	0.029
<input type="checkbox"/> tr	<u>Q9L8L1</u>	Exported serine protease SigA [sigA] [Shigella flexner...	42	0.029
<input type="checkbox"/> tr	<u>Q7C013</u>	Serine protease [sigA] [Shigella flexneri]	42	0.029
<input type="checkbox"/> tr	<u>Q8UJW1</u>	Autotransporter protein [yapE] [Agrobacterium tumefaci...	40	0.14
<input type="checkbox"/> tr	<u>Q7D396</u>	AGR_pAT_528p [AGR_pAT_528] [Agrobacterium tumefaciens ...	40	0.14
<input type="checkbox"/> tr	<u>Q7WK90</u>	Autotransporter [phg] [Bordetella bronchiseptica (Alca...	40	0.19
<input type="checkbox"/> tr	<u>Q7W8X9</u>	Autotransporter [phg] [Bordetella parapertussis]	40	0.19
<input type="checkbox"/> tr	<u>Q84GK0</u>	Secreted autotransporter protein EatA [eatA] [Escheric...	40	0.19
<input type="checkbox"/> tr	<u>Q8UJX1</u>	Autotransporter protein [bapA] [Agrobacterium tumefaci...	39	0.25
<input type="checkbox"/> tr	<u>Q7D3A2</u>	AGR_pAT_511p [AGR_pAT_511] [Agrobacterium tumefaciens ...	39	0.25
<input type="checkbox"/> tr	<u>Q6MTD5</u>	Hypothetical transmembrane protein [MSC_0473] [Mycopla...	39	0.32
<input type="checkbox"/> sp	<u>P45386</u>	IGA4_HAEIN Immunoglobulin A1 protease precursor (EC 3....)	39	0.42
<input type="checkbox"/> tr	<u>Q9Z5R3</u>	Phg protein (Autotransporter) [phg] [Bordetella pertus...	38	0.55
<input type="checkbox"/> tr	<u>Q6KD18</u>	Antigen 43 precursor Sap [sap] [Escherichia coli]	38	0.71
<input type="checkbox"/> tr	<u>Q8FDW4</u>	Acreceted auto transpoter toxin [sat] [Escherichia coli...]	37	1.2

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits 
Pfam hits  **Autotransporter** 



Alignments

tr Q51112 Similar to *Shigella flexneri* VirG protein (Fragment) 682
 [Neisseria meningitidis] AA align

Score = 1367 bits (3538), Expect = 0.0
 Identities = 669/682 (98%), Positives = 669/682 (98%)

Query: 1 QRKIYYETRXXXXXXXXXXXXIVSLFFSILYTSPLLAVIDYVYDKTKLTNDEITRLKKLR 60
 QRKIYYETR IVSLFFSILYTSPLLAVIDYVYDKTKLTNDEITRLKKLR
 Sbjct: 1 QRKIYYETRSKQASKQFKKSFIVSLFFSILYTSPLLAVIDYVYDKTKLTNDEITRLKKLR 60

Query: 61 DKTSEWKKETYLITEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR 120
 DKTSEWKKETYLITEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR
 Sbjct: 61 DKTSEWKKETYLITEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR 120

Query: 121 GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN 180
 GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN
 Sbjct: 121 GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN 180

Query: 181 SHINSEILSVGNYTEWANQVIHHIENYVFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD 240
 SHINSEILSVGNYTEWANQVIHHIENYVFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD
 Sbjct: 181 SHINSEILSVGNYTEWANQVIHHIENYVFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD 240

Query: 241 EFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT 300
 EFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT
 Sbjct: 241 EFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT 300

Query: 301 ALIFEKNVTGTSIIIFENPIDDLSKSLDGHQIIVNGTADKHAFRLSGKHQKGIYTLSLQQ 360
 ALIFEKNVTGTSIIIFENPIDDLSKSLDGHQIIVNGTADKHAFRLSGKHQKGIYTLSLQQ
 Sbjct: 301 ALIFEKNVTGTSIIIFENPIDDLSKSLDGHQIIVNGTADKHAFRLSGKHQKGIYTLSLQQ 360

Query: 361 RPEGFLPKCKNAMIWRFMHNRKPPIPYCALRLNNKNSIDFRTLPRKGLWLRVIDGHSN 420
 RPEGFLPKCKNAMIWRFMHNRKPPIPYCALRLNNKNSIDFRTLPRKGLWLRVIDGHSN
 Sbjct: 361 RPEGFLPKCKNAMIWRFMHNRKPPIPYCALRLNNKNSIDFRTLPRKGLWLRVIDGHSN 420

Query: 421 QWVQGKTAPEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGN 480
 QWVQGKTAPEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGN
 Sbjct: 421 QWVQGKTAPEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGN 480

Query: 481 VKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDTERFTSKGITASIEAGYN 540
 VKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDTERFTSKGITASIEAGYN
 Sbjct: 481 VKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDTERFTSKGITASIEAGYN 540

Query: 541 ALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNKGFSDENAHVNLGSRQLQTRGVQAKAQ 600
 ALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNKGFSDENAHVNLGSRQLQTRGVQAKAQ
 Sbjct: 541 ALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNKGFSDENAHVNLGSRQLQTRGVQAKAQ 600

Query: 601 FSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQAT 660
 FSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQAT
 Sbjct: 601 FSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQAT 660

Query: 661 FNRQTGKHHQAKQGALNLQWTF 682
 FNRQTGKHHQAKQGALNLQWTF
 Sbjct: 661 FNRQTGKHHQAKQGALNLQWTF 682

tr Q9JTL4 Putative virulence associated protein [NMA1725] [Neisseria meningitidis (serogroup A)]

align

Score = 1043 bits (2698), Expect = 0.0

Identities = 529/650 (81%), Positives = 568/650 (87%), Gaps = 12/650 (1%)

Query: 37 LAVDYVYDKTLNDEITRLKKLRDKTSEYWKKETYLITEDNPKVPPFPALYPRY--QF 94
+AVDYVYDKTLT+DEITRLKKLRD+ SEYWK+ETY I +N P PAL+P+ F

Sbjct: 1 MAVDYVYDKTLNDEITRLKKLRDRNSEYWEETYHIKSNNRVPNIPALFPKHPFDPF 60

Query: 95 ENINNSKKISFYDQEYTEGYLGVFARGLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYST 154
ENINNSK+ISFYD+EYTE YLVGFA+GLGVAKRNG+TE+ IR+YFKEC N+ D T

Sbjct: 61 ENINNSKRISFYDKEYTEDYLVGFAQGLGVAKRNGETEKPIRQYFKECLNTGKYSDD--T 118

Query: 155 CQAEGFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQVIIHENYVFAAHL 214
C++++ S P V+S IF+L KIKNSHINSEILSVGNY EW ++ + S HL

Sbjct: 119 CKSQQ--SIPT-VRSDIFALNTKIKNSHINSEILSVGNYIEWLRPTLNQLS---SSQEHL 172

Query: 215 YSGLDPFHYIEVTDNSHVIGQTISLDEFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSE 274
YS +DPFH YIEVTDNSHVIGQTISLDEFRLENSLWEPRWDS+VG+LTTNADIRFNTKSE

Sbjct: 173 YSDVDPFHYIEVTDNSHVIGQTISLDEFRLENSLWEPRWDSVGEKTTNADIRFNTKSE 232

Query: 275 SLLVKEDYAGGARFRFAYDPKEA--KNTALIFEKNVTGTSIIIFENPIDDLKSLDGHQII 332
SLLVKEDYAGGARFRFAY K+ + L FEKN+TGTSIIIFENPIDDLKSLDGHQII

Sbjct: 233 SLLVKEDYAGGARFRFAYGLKDKVPETPVLTFEKNITGTSIIIFENPIDDLKSLDGHQII 292

Query: 333 KVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNLKPPIPYCALR 392
KVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGF K + + + ALR

Sbjct: 293 KVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFFTQERDDISIYAQQQAANTLFALR 352

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQ 452
LN+KNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVE RKGVQLGGEVFTWQNESNQ

Sbjct: 353 LNDKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVESNRKGVQLGGEVFTWQNESNQ 412

Query: 453 LSIGLMGGQAEQRSTFHNPDTNDLTTGNVKFGAGVYATWHQLQDKQTGAYADSWMQR 512
LS+GLM GQAEQRSTF NPDTNDLTTGNVKFGAG+YATWHQLQDKQTGAYADSW+QYQR

Sbjct: 413 LSVGLMSGQAEQRSTFRNPDTNDLTTGNVKFGAGIYATWHQLQDKQTGAYADSWVQYQR 472

Query: 513 FRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
FRHRINTED TERFTSKGITASIEAGYNALLAEHFTKKGN +R YLQPQAQLTYLGVNGK

Sbjct: 473 FRHRINTEDATERFTSKGITASIEAGYNALLAEHFTKKGNRVRFYLQPQAQLTYLGVNGK 532

Query: 573 FSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGER 632
FSDSENAHVNLGSRQLQ+RVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGER

Sbjct: 533 FSDSENAHVNLGSRQLQSRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGER 592

Query: 633 RVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682

R+INNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF

Sbjct: 593 RMINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF, 642

tr Q6Q509

Lav (Fragment) [Haemophilus influenzae]

695 AA

align

Score = 962 bits (2486), Expect = 0.0
 Identities = 494/665 (74%), Positives = 547/665 (81%), Gaps = 13/665 (1%)

Query: 23 IVSLFFSILYTSPLLAV-DYVYDKTKLTNDEITRLKKLRDKTSEYWKKETYLITEDNPKV 81
 ,I+SLFFSILYTSPLLAV DY YD +KLTN++I RLKKLRD+ SEYWKKETYL+
 Sbjct: 39 IIISLFFSILYTSPLLAVVDTYDNTSKLTNEQIERLKKLRDRNSEYWKKETYLLKSPPSNF 98

Query: 82 PPFPALYPR--TYQFENINNSKKISFYDQEYTEGYLVGFARGLGVAKRNGDTEEQIRKYF 139
 P P L+P+ + FENI+NSK ISFYDQ+YTE YLVGFA+G GVAKRNGDTEE +RKYF
 Sbjct: 99 PDIPVLFPKDSSVPFENIDNSKAISFYDQKYTEDYLVGFAQGFGVAKRNGDTEEPVRKYF 158

Query: 140 KECFNSNTKIRDYSTCQAEGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQ 199
 KEC N+ D C+A S + +KS IF+ P IKNSHINSEIL+VGNYTE
 Sbjct: 159 KECLNTGNYNND--NCKANPLASS-VSIKSDIFTPRPTIKNSHINSEILAVGNYTEL--- 212

Query: 200 VIHHIENYVSFAAHLYSGLDPHYIEVTDNSHVIGQTISLDEFRLENSWEPRWDSNVKG 259
 ++ + S+A HLYS DP + V DNSHVIGQTI L +L NSLWEPRW+SN+
 Sbjct: 213 MLAAQPSASSWAELHLYS--DPGLSLTVQDNSHVIGQTIDLGFLQLTNSLWEPRWNSNIDY 270

Query: 260 LKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEA--KNTALIFEKNVTGTSIDIIFE 317
 L T NA+IRFNTK+ESLLV+ YAGGARFRFAYD K+ + L FE+N+TGTSDIIFE
 Sbjct: 271 LVTENAEIRFNTKNESSLVEGYYAGGARFRFAYDLKDQAPETPVLTFEQNITGTSIDIIFE 330

Query: 318 NPIDDLKSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRF 377
 NPIDDLKSLDGHQI+KVNGTADK+AFRLSGK++KGIYTLSLQQR EGF K +
 Sbjct: 331 NPIDDLKSLDGHQIVKVNGTADKNAFRLSGKYRKGIYTLSLQQRLEGFFTQLQERDDIAI 390

Query: 378 MHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGV 437
 + + ALRLN+KNSDIFDRTLPRKGLWLRVIDGHS+QWVQGKTAP+EGYRKGV
 Sbjct: 391 YAQQQAQANTLFALRLNDKNSDIFDRTLPRKGLWLRVIDGHSSQWVQGKTAPLEGYRKGV 450

Query: 438 QLGGEVFTWQNESNQLSIGLMMGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQD 497
 QLGGEVFTWQNESNQ S+GLMGGQAEQRSTF NPDTDNLTGNG+KG GAGVYATWHQLQD
 Sbjct: 451 QLGGEVFTWQNESNQFSVGLMMGQAEQRSTFRNPDTDNLTGNGMKGAGVYATWHQLQD 510

Query: 498 KQTGAYADSWMQYQRFRHINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVY 557
 KQTGAY DSW QYQRFRHINTEDGTERFTSKGITASIEAGYNALLAEH T KG +R Y
 Sbjct: 511 KQTGAYVDSWAQYQRFRHINTEDGTERFTSKGITASIEAGYNALLAEHTGKGTQIRFY 570

Query: 558 LQPQAQLTYLGVNGKFDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNA 617
 LQPQAQLTYLGVNGKFDSEN+ VNLLGSRQLQ+RVGVQAKAQF L KNI I+PFAAVN
 Sbjct: 571 LQPQAQLTYLGVNGKFDSENSQVNLLGSRQLQSRGVQAKAQFLLKNIVIQPFAAVNT 630

Query: 618 LYHNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALN 677
 LYH+KPGVEMDGERRVINNKTAIESQ G+AVKIKSHLTLQATFNRQTGKHH AKQGALN
 Sbjct: 631 LYHSKPGVEMDGERRVINNKTAIESQFGIAVKIKSHLTLQATFNRQTGKHHAKQGALN 690

Query: 678 LQWTF 682
 LQWTF
 Sbjct: 691 LQWTF 695

tr Q93N95 Lav (Fragment) [lav] [Haemophilus influenzae] 692 AA
align

Score = 954 bits (2467), Expect = 0.0

Identities = 487/664 (73%) , Positives = 543/664 (81%) , Gaps = 13/664 (1%)

Query: 23 IVSLFFSILYSPPLLAVDYYDKTKLTNDEITRLKKLRDKTSEYWKKETYLITEDNPKVP 82
I+SL S LY+SPPLLAVDYYDKTKLT+DEITRLKKLRD+ SEYWK+ETY I P

Sbjct: 38 ILSLLVSALYSSPLLAVDYYDKTKLTDEITRLKKLRDRDSEYWKEETYFIKSTPQSPP 97

Query: 83 PFPALYPRTY--QFENINNSKKISFYDQEYTEGYLVGFARGLGVAKRNGDTEEQIRKYFK 140
P L+P+ FENINNSK+ISFYD+E+TE YLVGFA+G GVAKRNG+TEE +R+YFK

Sbjct: 98 NIPRLFPKNSFDSFENINNSKEISFYDKEFTEDYLVGFAQGFGVAKRNGEETEVRQYFK 157

Query: 141 ECFNSNTKIRDYSTCQAEEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQV 200
EC N+ D TC++ + + +KS IF+L +KNSHINSEIL+VGNYT+

Sbjct: 158 ECLNTGKHSND-PTCKS--YSTDAYNIKSDIFALNTIVKNSHINSEILAVGNYTKMLSA 214

Query: 201 IHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLDEFRLENSLWEPRWDSNVGKL 260
H + + A HLYS + + V DNSHVIGQTI L L NSLWEPRW+SN+ L

Sbjct: 215 QHSS----TWAEHLYSNAELS--LTVQDNSHVIGQTIDLGALILTSNLWEPRWNSNIDYL 268

Query: 261 KTTNADIRFNTKSESLLV ред YAGGARFRFAYD--PKEAKNTALIFEKNTGTSIIFEN 318
T NADIRFNTKSESLLV ред +YAGGARFRFAYD K + L FE+N+TGTSDIIFEN

Sbjct: 269 ATENADIRFNTKSESLLV ред KGNYAGGARFRFAYDLQDKAPETPVLTFEQNITGTSIIFEN 328

Query: 319 PIDLKSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFM 378
PID+LKSLDGHQI+KVNGTADK+AFRLSGK++KGIYTLSLQ+RPEGF K +

Sbjct: 329 PIDNLKSLDGHQIVKVNGTADKNAFRRLSGKYRKGIYTLSLQRRPEGFFTKVQERDNIAIY 388

Query: 379 HNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQ 438
+ + ALRLN+KNSDIFDRTLPRKGLWLRVIDGHS+QWVQGKTAP+EGYRKGVQ

Sbjct: 389 AQQAQAANTLFALRLNDKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPLEGYRKGVQ 448

Query: 439 LGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQLQDK 498
LGGEVFTWQNESNQ S+GLMGGQAEQRSTF NPDTNDLTTGN+KGFGAGVYATWHQLQDK

Sbjct: 449 LGGEVFTWQNESNQFSVGLMGGQAEQRSTFRNPDTNDLTTGNMKGFGAGVYATWHQLQDK 508

Query: 499 QTGAYADSWMQYQRFRHINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYL 558
QTGAY DSW+QYQRFRH INTEDGTERFTSKGITASIEAGYNALLAEH T KG +R YL

Sbjct: 509 QTGAYIDSWVQYQRFRHINTEDGTERFTSKGITASIEAGYNALLAEHTGKGTQIRFYL 568

Query: 559 QPQAQLTYLGNGKFSDENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNL 618
QPQAQLTYLGNGKFSDESEN+ VNLLG RQLQ+RVGQAKAQF L KNI I+PFAAVN L

Sbjct: 569 QPQAQLTYLGNGKFSDESENQVNLLGPRQLQSRGVQAKAQFLLNKNIVIQPFAAVNL 628

Query: 619 YHNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNL 678
YH+KPGVEMDGERRVINNKTAIESQ G+AVKIKSHLTLQATFNRQTGK H AKQGALNL

Sbjct: 629 YHSKPGVEMDGERRVINNKTAIESQFGIAVKIKSHLTLQATFNRQTGKHHAKQGALNL 688

Query: 679 QWTF 682

QWTF

Sbjct: 689 QWTF 692

tr Q93N94 Las (Fragment) [las] [Haemophilus influenzae biotype
aegyptius] 703
AA
align

Score = 663 bits (1710), Expect = 0.0

Identities = 337/480 (70%), Positives = 386/480 (80%), Gaps = 5/480 (1%)

Query: 204 IENYVSFAAHLYSGLDPFHYSIEVTDNSHVIGQTISLDEFRLLENSLWEPRWDSNVGKLKTT 263
I+NY S GL + V + S V G T+ L + L++SLWEPR++S+V L+T
Sbjct: 228 IDNYRSKFPDETRGLT---LTVKNQSEVRGATLQLLKMVLQDSLWEPRFNSDVHLETQ 283

Query: 264 NADIRFNTKSESLLVKEDYAG-GARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDD 322
NA+IRFN+ + L V E+Y G G+RF ++PKEA L F+K+VTGTS+I+FE PIDD
Sbjct: 284 NANIRFNSTNTRLTVHENYQGDGSRFFIKFNPKEATQPVLTFDKDVTGTSNIVFEKPIDD 343

Query: 323 LKSLDGHQI1KVNGTADKHAFLSGKHQKG1YTLQLQQRPEGFLPKCKNAMIWRFMHNRL 382
LKSLDGHQI1KVNGTADKHAFLSGKHQKG1YTLQLQQRPEGF K + +
Sbjct: 344 LKSLDGHQI1KVNGTADKHAFLSGKHQKG1YTLQLQQRPEGFFTKVQERDDIAIYAQQA 403

Query: 383 KPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGE 442
+ ALRLN+KNSDIFDRTLPRKGLWLR+I GH +Q VQGKTAPVEG RKG+QLGG+
Sbjct: 404 QAANTLFALRLNDKNSDIFDRTLPRKGLWLRЛИSGHLSQDVQGKTAPVEGNRKG1QLGGD 463

Query: 443 VFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVYATWHQLQDKQTGA 502
VF+ QN+ QLS GLMGGQAEQRSTF N DTDNLTTG++KFGAG+YATWHQLQDKQTGA
Sbjct: 464 VFSLQNQDYQLSFGLMGGQAEQRSTFRNSDTDNLTTGSMKGFGAGIYATWHQLQDKQTGA 523

Query: 503 YADSWMQYQRFRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLPQQA 562
Y DSW+QYQRFRHRINTEDG ERTTSKGITASIEAGYNALLAEH T+KG +R YLQPOQA
Sbjct: 524 YVDSWVQYQRFRHRINTEDGIERFTSKGITASIEAGYNALLAEHLTEKGTQIRFYLPQQA 583

Query: 563 QLTYLGVNGKFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNK 622
QLTYLGVNG +DS N+ VNLLGSRQL+RVG QAKAQF+ + +PF A+N++Y K
Sbjct: 584 QLTYLGVNGDLTDGNSKVNLGSRQLQSRVGAQAKAQFTFTNGVIFQPFVALNSIYQQK 643

Query: 623 PFGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682
PFGVE+D ERRVINNKTAIESQLGVA+KIKSHLTLQATFNRQTGKHH AKQGALNLQWTF
Sbjct: 644 PFGVEIDNERRVINNKTAIESQLGVALKIKSHLTLQATFNRQTGKHHAKQGALNLQWTF 703

tr Q9JPL5 Autotransporter A [autA] [Neisseria meningitidis] 619 AA align

Score = 389 bits (1000), Expect = e-107
Identities = 207/471 (43%), Positives = 302/471 (63%), Gaps = 24/471 (5%)

Query: 223 YIEVTDNSHVIGQTISLDEFRLLENSLWEPRWDSNVGKLKTT-NADIRFNTKSESLLVKED 281
++++ + SHV GQ + L + L++SLWEPR S++ L+T+ NA IR NTK E L V +D
Sbjct: 162 HVKIENKSHVAGQVLELTKMTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKD 221

Query: 282 YAGGARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDDLKSLDGHQI1KVNGTADKH 341
YAGGA F F YD +E+ AL FE V+G S ++ E ++LK+LDG ++I TAD
Sbjct: 222 YAGGADFLFGYDVRESDEPALTFEDKVSGQSGVVLERPENLKTLDGRKLIAAK-TADSG 280

Query: 342 AFRLSGKHQKG1YTLQLQQRPEGF-----LPKCKNAMIWR-FMHNRLKPPPIPYCAL 391
+ + +G+Y L L+Q GF +P+ + + + N L L
Sbjct: 281 SLAFKQNYRQGLYELLKQCEGGFCLGVQRLAYPEAEAVLYAQQAYAANTL-----FGL 334

Query: 392 RLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESN 451
R ++ D++ R+ LWLR I G S+Q ++G A +G+RKGVQ+GGEVF QNE +
Sbjct: 335 RAADRGDDVYAADPSRQKLWLRFIGGRSHQNIRGGAA-ADGWRKGVQIGGEVFVRQNEGS 393

Query: 452 QLSIGLMGGQAEQRSTFHNPDTDNLLTGNVKFGAGVYATWHQLQDKOTGAYADSMQYQ 511
 +L+IG+MGG+A Q ++ + ++ G+G GVYA WHQL+DKQTGAY D W+QYQ
 Sbjct: 394 RLAIGVMGGRAGQHASVNGKG--GAAGSDLYGYGGGVYAAWHQLRDQKQTGAYLDGWLQYQ 451

Query: 512 RFRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPAQLTYLGVNG 571
 RF+HRIN E+ ER+ +KG TAS+E GYNAL+AE KGN++R YLQPQAQ TYLGVNG
 Sbjct: 452 RFKHRINDENRAERYKTKGWTASVEGGYNALVAEGIVGKGNNVRFYLQPAQFTYLGVNG 511

Query: 572 KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGE 631
 F+DSE V LLGS Q Q+R G++AK F+L + ++PFAA N L+ +K FGVEMDGE
 Sbjct: 512 GFTDSEGTAVGLLGSGQWQSRAKIRAKTRFALRNGVNLQPFAAFNVLHRSKSGVEMDGE 571

Query: 632 RRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTKHHQAKQGALNLQWT 682
 ++ + +TA+E + G+ K H++ + + ++T K+ AL+L+W F
 Sbjct: 572 KQTLAGRATALEGRCIEAGWKGHMSARIGYKRTDGD---KEAALSLKWL 619

tr Q9ZF58 *Virulence-associated protein VapA [vapA] [Neisseria meningitidis]* 619
 AA
align

Score = 388 bits (997), Expect = e-106
 Identities = 224/576 (38%), Positives = 338/576 (57%), Gaps = 46/576 (7%)

Query: 130 DTEEQIRKYFKECFNSNTK----IRDYSTCQAEKFGSHPLIVK-SHIFSLGPKI--- 178
 D ++KY + + N K ++D + E + + + ++I LGPK
 Sbjct: 67 DNMPVVKKYITDTYGDNLKDAVKKQLQDLYKTRPEAWEENKRTEEAYIEQLGPKFSLK 126

Query: 179 -KNSHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHIEVTDNSHVIGQTI 237
 KN + + + + T + N + N + H + + + + SHV GQ +
 Sbjct: 127 QKNPDLINKLVEDSVLTPHSNTSQTSNNIFNKKLH-----VKIENKSHVAGQVL 176

Query: 238 SLDEFRLENSWEPRWDNSVKGKLTT-NADIRFNTKSESLLVKEDYAGGARFRFAYDPKE 296
 L + L++SLWEPR S++ L+T+ NA IR NTK E L V + Y GGA F F YD +E
 Sbjct: 177 ELTKMTLKDSLWEPRRHSDIHTLETSNARIRLNTKDEKLTvhkayQGGADFLFGYDVRE 236

Query: 297 AKNTALIFEKNVTGTSIIIFENPIDDLKSLDGHQIIKVNGTADKHAFRLSGKHQKGITYL 356
 + AL FE+NV+G S+++ E ++LK+LDG ++I AD. ++F + + +G+Y L
 Sbjct: 237 SDEPALTFEQNVSGKSNVVERPENLKTLDGRKLIAAE-KADPNSFAFKQNYRQGLYEL 295

Query: 357 SLQQRPEGF-----LPKCKNAMIWR--FMHNRLKPPIPYCALRLNNKNSIFDRTLP 406
 L+Q GF +P+ + + + N L LR ++ D++
 Sbjct: 296 LLKQCEGGFCLGVQRLAIPEAEAVLYAQQAYAANTL-----FGLRAADRGDVYAADPS 349

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGEVFTWQNESNQLSIGLMGGQAEQRS 466
 R+ LWLR I G S+Q ++G A +G RKGVQ+GGEVF QNE ++L+IG+MGG+A Q +
 Sbjct: 350 RQKLWLRFIGGRSHQNIRGGAA-ADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHA 408

Query: 467 TFHNPDTDNLLTGNVKFGAGVYATWHQLQDKQTGAYADSMQYQRFRHINTEDGTERF 526
 + + + G+G GVYA WHQL+DKQTGAY D W+QYQRF+HRIN E+ ER+
 Sbjct: 409 SVNGKG--GAAGSYLHGYYYAAWHQLRDQKQTGAYLDGWLQYQRFKHRINDENRVERY 466

Query: 527 TSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPAQLTYLGVNGKFSDENAHVNLGS 586
 +KG TAS+E GYNAL+AE KGN++R YLQPQAQ TYLGVNG F+DSE V LLGS
 Sbjct: 467 KTKGWTASVEGGYNALVAEGVVGKGNNVRFYLQPAQFTYLGVNGGFTDSEGTAVGLLGS 526

Query: 587 RQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLG 646
 Q Q+R G++AK +F+L + ++PFAA N L+ +K FGVEMDGE++ + +TA+E + G
 Sbjct: 527 GQWQSRAKTRFALRNGVNLQPF-AAFNVLHRSKSFVEMDGEKQTLAGRTALEGRFG 586

Query: 647 VAVKIKSHLTLQATFNRQTKHHQAKQGALNLQWTF 682
 + K H+ + + ++T K+ AL+L+W F
 Sbjct: 587 IEAGWKGHMFARIGYGKRTDGD---KEAALSLKWL 619

tr Q9JSR2 Putative virulence associated protein [vapA] 619 AA
 [Neisseria align
 meningitidis (serogroup A)]

Score = 387 bits (993), Expect = e-106
 Identities = 223/576 (38%), Positives = 337/576 (57%), Gaps = 46/576 (7%)

Query: 130 DTEEQIRKYFKECFNSNTK-----IRDYSTCQAEEKFGSHPLIVK-SHIFSLGPKI---- 178
 D + +KY + + N K + +D + E + + + + +I LGPK
 Sbjct: 67 DNMPVVKKYITDTYGDNLKDAVKKQLQDLYKTRPEAEEENKKRTEEAYIEQLGPKFSLK 126

Query: 179 -KNSHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHIEVTDNSHVIGQTI 237
 KN + + + + T + N + N + H + + + + SHV GQ +
 Sbjct: 127 QKNPDLINKLVEDSVLTPEHSNTSQTSLNNIFNKKLH-----VKIENKSHVAGQVL 176

Query: 238 SLDEFRLENSWEPRWDSNVGKLTT-NADIRFNTKSESLLVKEDYAGGARFRFAYDPKE 296
 L + L++SLWEPR S++ L+T+ NA IR NTK E L V + Y GGA F F YD +E
 Sbjct: 177 ELTKMTLKDSDLWEPRRHSDIHMLETSDNARIRLNKDEKLTVHKAYQGGADFLFGYDVRE 236

Query: 297 AKNTALIFEKNVTGTSIIIFENPIDDLSKSLDHQIIVNGTADKHAFRLSGKHQKGIYTL 356
 + AL FE+ V+G S ++ E + +LK+LDG + +I AD + +F + + +G+Y L
 Sbjct: 237 SDKPALTFEEKVSGQGVVLERPENLKTLDGRKLIAAE-KADSNFAFKQNYRQGLYEL 295

Query: 357 SLQQRPEGF-----LPKCKNAMIWR--FMHNRLKPPIPYCALRNNKNSDIFDRTLP 406
 L+Q GF +P+ + + + + N L LR + + D++
 Sbjct: 296 LLKQCEGGFCLGVQRLAYPEAEAVLYAQQAAYAANTL-----FGLRAADRGDDVYAADPS 349

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRS 466
 R+ LWLR I G S+Q ++G A +G RKGVQ+GGEVF QNE ++L+IG+MGG+A Q +
 Sbjct: 350 RQKLWLRFIGGRSHQNIRGGAA-ADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHA 408

Query: 467 TFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQGTGAYADSWMQYQRFRHRINTEDGTERF 526
 + + + G+G GVY WHQL+DKQTGAY D W+QYQRF+HRIN E+ ER+
 Sbjct: 409 SVNGKG--GAAGSYLHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERY 466

Query: 527 TSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDENAHVNLGS 586
 +KG TAS+E GYNAL+AE KGN++R YLQPQAQ TYLGVNG F+DSE V LLGS
 Sbjct: 467 KTKGWTASVEGGYNALVAEGVVGKGNNVRFYLQPQAQFTYLGVNGGFTDSEGTAVGLLGS 526

Query: 587 RQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLG 646
 Q Q+R G++AK +F+L + ++PFAA N L+ +K FGVEMDGE++ + +TA+E + G
 Sbjct: 527 GQWQSRAKTRFALRNGVNLQPF-AAFNVLHRSKSFVEMDGEKQTLAGRTALEGRFG 586

Query: 647 VAVKIKSHLTLQATFNRQTKHHQAKQGALNLQWTF 682
 + K H+ + + ++T K+ AL+L+W F
 Sbjct: 587 IEAGWKGHMSARIGYGKRTDGD---KEAALSLKWL 619

tr Q6J5G0 Putative virulence-associated protein (Fragment) [Haemophilus influenzae]

align

Score = 219 bits (557), Expect = 2e-55

Identities = 136/291 (46%), Positives = 165/291 (55%), Gaps = 47/291 (16%)

Query: 235 QTISLDEFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSESLLVKE----- 280
Q I L E L E N S L W E P R W D S + V L N + I R F N T K + E S L + V E

Sbjct: 1 QVIHLYELNLENSLWEPRWDSVSYLSLYNSHIRFNTKNESLVVGGENRIRPTPDNALETE 60

Query: 281 -----DYA-GGARFRFAYD--PKEAKNTALIFEKNVTGTS 312
DY G RFAYD +EA L + V G +

Sbjct: 61 KDFKSRFSNIGYHSSSKITISYNNNSRDYVLGYP SIRFAYDL SEREADKPVLTLKSKVRGKT 120

Query: 313 DII FENP-IDDLKSLDGHQIIKVNGTADKHA FRLSGKHQKGIYTLSLQQRPEGFLPKCKN 371
I+FE + + + LK+L Q+IK + AF L + + + KG Y L LQO P GF +

Sbjct: 121 AIVFEEKALNNLKNLTYRQLIKTETDIEPD AFFLLEEYKKGRYRLFIQQCPNGFCIGVEK 180

Query: 372 AMIWRFM---HNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKT 427
I + + + + ALRLN+KNSDIFDRTLPRKGLWLR+I GH +Q VQGKT

Sbjct: 181 LAIPTHLVASYAQQAQAANTLFALRLNDKNSDIFDRTLPRKGLWLR L ISGHL SQDVQGKT 240

Query: 428 APVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTT 478

APVEG RKG+QLGG+VF+ QN+ Q S GLMGGQAEQRSTF NPDT N+TT

Sbjct: 241 APVEGNRKGIQLGGDVFSLQNQDYQFSFGLMGGQAEQRSTFRNPDTGNVTT 291

tr Q8X6C1 Putative beta-barrel outer membrane protein [z0402]

1349

[Escherichia coli]

AA

0157:H7]

align

Score = 142 bits (359), Expect = 2e-32

Identities = 100/327 (30%), Positives = 156/327 (47%), Gaps = 31/327 (9%)

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGK-TAP 429
N M +H RL N +D+ + +W+R GH N+W G

Sbjct: 1039 NTMFTTRLHERLG-----NTYYTDMVTGEQKQTTMWMRHEGGH-NKWRDGSGQLK 1087

Query: 430 VEGYRKGVQLGGEVFTW-QNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGV 488
+ R +QLGG+V W QN S++ +G+M G S + T +V G+ G+

Sbjct: 1088 TQSNRYVLQLGGDVAQWSQNGSDRWHGVGMAGYGNSDSKTISSRTGYRAKASVNGYSTGL 1147

Query: 489 YATWHQLQDKQTGAYADSWM QYQRFRH RINTED-GTERFTSKGITASIEAGYNALLAEHF 547
YATW+ + + GAY DSW QY F + + +D +E + SKG TAS+EAGY LAE

Sbjct: 1148 YATWYADDES RNGAYLDSWAQYSWFDNTVKGDDLQSESYKSKGFTASLEAGYKHKLA EFN 1207

Query: 548 TKKGNSLRVYLPQPAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQ A--KAQFSL- 603
+G Y+QPQAQ+T++GV K +S V+ G +QTR+GV+ K+ +

Sbjct: 1208 GSQGTRNEWYVQPQAQVTWMGVKADKHRESNGTLVHSNGDGNVQTRLGVKTWLKSHHKMD 1267

Query: 604 -YKNIAIEPFAAVNALYHNKPFGVEM-----DGERRVINNKTAIESQLGVAVKIKSHL 655
K+ +PF VN L+++K F M DG R + KT +E QL + + ++

Sbjct: 1268 DGKSREFQPFPVEVNWLHNSKDFSTSMGVSVTQDGARNIAEIKTGVEGQLNANLNWGNV 1327

Query: 656 TLQATFNRQTGKHHQAKQGALNLQWTF 682

+Q + + + ++W F

Sbjct: 1328 GVQV-----ADRGYNDTSAMVGIKWQF 1349

tr Q7AH89 AidA-I adhesin-like protein [ECs0362] [Escherichia coli] 1327
0157:H7 AA align

Score = 142 bits (359), Expect = 2e-32

Identities = 100/327 (30%), Positives = 156/327 (47%), Gaps = 31/327 (9%)

Query: 371 NAMIWRFMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGK-TAP 429
N M +H RL N +D+ + +W+R GH N+W G

Sbjct: 1017 NTMFTTRLHERLG-----NTYYTDMVTGEQKQTTMWMRHEGGH-NKWRDGSGQLK 1065

Query: 430 VEGYRKGVQLGGEVFTW-QNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGKFGAGV 488
+ R +QLGG+V W QN S++ +G+M G S + T +V G+ G+

Sbjct: 1066 TQSNRYVLQLGGDVAQWSQNGSDRWHGVGMAGYGNSDSKTISSRTGYRAKASVNGYSTGL 1125

Query: 489 YATWHQLQDKQTGAYADSWMQMQRFRHINTED-GTERFTSKGITASIEAGYNALLAEHF 547
YATW+ + + GAY DSW QY F + + +D +E + SKG TAS+EAGY LAE

Sbjct: 1126 YATWYADDESRNGAYLDSWAQYSWFDNTVKGDDLQSESYKSKGFTASLEAGYHKLAEFN 1185

Query: 548 TKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQA--KAQFSL- 603
+G Y+QPQAQ+T++GV K +S V+ G +QTR+GV+ K+ +

Sbjct: 1186 GSQGTRNEWYVQPQAQVTWMGVKADKHRESNGTLVHSNGDGNVQTRLGVKTLKSHHKMD 1245

Query: 604 -YKNIAIEPFAAVNALYHNKPGVEM-----DGERRVINNKTAIESQLGVAVKIKSHL 655
K+ +PF VN L+++K F M DG R + KT +E QL + + ++

Sbjct: 1246 DGKSREFQPFPVEVNWLHNSKDFSTSMGVSVTQDGARNIAEIKTGVEGQLNANLNWGNV 1305

Query: 656 TLQATFNRQTGKHHQAKQGALNLQWTF 682

+Q + + + ++W F

Sbjct: 1306 GVQV-----ADRGYNDTSAMVGIKWQF 1327

tr Q6KCW6 YapH homolog [yapH] [Escherichia coli] 2001 AA align

Score = 139 bits (351), Expect = 1e-31

Identities = 87/294 (29%), Positives = 145/294 (48%), Gaps = 10/294 (3%)

Query: 398 SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA-PVEGYRKGVQLGGEVFTWQNESNQLSIG 456
+D+F +W+R I GH N+W + + R VQLGG + W + ++L G

Sbjct: 1709 TDVFTGEKKATSMWMRHIGGH-NRWKDSSSQLNTQSNRYVVQLGGSIAQWTDGQDRLQQG 1767

Query: 457 LMGGQAEQRSTFHNPDTDNLTGKFGAGVYATWHQLQDKQTGAYADSWMQMQRFRHR 516
+M G ++S+ + + + G + G+ G+Y TW Q GAY D+W+QY F +

Sbjct: 1768 IMAGYGNESSTTSSLGYKSKGAIINGYSTGLYGTWQQNDGNDNGAYVDTWIQYGFNNNT 1827

Query: 517 INTED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFS 574
+N E E + S+G T S+EAGY E +G+ Y+QPQ+Q+T++ V + +

Subjct: 1828 VNGEKLAESWKSRGFTGSVEAGYTFKAGEFTGSQGSHYDWTYIQPQSQITWMNVRASEHT 1887

Query: 575 DSENAHVNLLGSRQLQTRGVV---QAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDG 630
+ V L G +Q+R+GV + K+ K EPF VN +++ + +GV+MD

Subjct: 1888 EKNGTKVQLSGDGNIQSRLGVRTYLKGKSASDDNKAHQFEPFVEVNWIHNTRSGVVKMDN 1947

Query: 631 ERRVINNKTAI-ESQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
+ T I E + GV K+ +L + Q G K + Q L +++ F

Subjct: 1948 TALSQDGATNIAEVKTVQGKLSNDLNWGNVQAGDKGYSDAQAMLGKTYIF 2001

tr Q8FFF9 Hypothetical protein ydeU [ydeU] [Escherichia coli] 291 AA
06] align

Score = 137 bits (344), Expect = 9e-31

Identities = 85/282 (30%), Positives = 141/282 (49%), Gaps = 10/282 (3%)

Query: 410 LWLRVIDGHSNQWVQGKTA-PVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTF 468
+W+R I GH N+W + + R VQLGG + W + ++L G+M G ++S+

Subjct: 11 MMWRHIGGH-NRWKDSSSQLNTQSNRYVVQLGGSIAQWTDGQDRLQQGIMAGYGNEKSST 69

Query: 469 HNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTED-GTERFT 527
+ + + G + G+ G+Y TW Q GAY D+W+QY F + +N E E +

Subjct: 70 TSSLGGYKSKGAINGYSTGLYGTWQNDGNDNGAYVDTWIQYGFNNTVNGEKLAESWK 129

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAOQLTYLGVN-GKFSDSENAHVNLGS 586
S+G T S+EAGY E +G+ Y+Q+P+Q+T++ V + ++ V L G

Subjct: 130 SRGFTGSVEAGYTFKAGEFTGSQGSHYDWTYIQPQSQITWMNVRASEHTEKNGTKVQLSGD 189

Query: 587 RQLQTRGVV---QAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAI- 641
+Q+R+GV + K+ K EPF VN +++ + +GV+MD + T I

Subjct: 190 GNIQSRLGVRTYLKGKSASDDNKAHQFEPFVEVNWIHNTRSGVVKMDNTALSQDGATNIA 249

Query: 642 ESQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682

E + GV K+ +L + Q G K + Q L +++ F

Subjct: 250 EVKTGVQGKLSNDLNWGNVQAGDKGYSDAQAMLGKTYIF 291

tr Q7BCK4 VirG [virG] [Shigella flexneri] 1102 AA
align

Score = 134 bits (338), Expect = 4e-30

Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT---LPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVF-TWQNESNQL 453
S I D T L +W+R + GH+ + + R Q+GG++ T + + L

Subjct: 806 STIVDPTTGQLSETTMWIRTVGGHNEHNLADRQLKTTANRMVYQIGGDILKTNFTDHGGL 865

Query: 454 SIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
+G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F

Subjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNGK 572
+ + + T E+++SKGIT ++EAGY +YL PQ Q+T GV

Subjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLNPPQVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLGSRQLQTRGVQAK--AQFSLYKNI--AIEPFAAVNALYHNKPFGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQAKGLRTSLISQSCIDKETLRKFEPPFLEVNWKSSKQYGV 1045

Query: 628 MDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRNVIELKTVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q99Q93 **IcsA (VirG), outermembrane protein exposed to the bacterial surface** 1102
 by a C-terminal autotransporter domain and involved in AA
 the movement of intracellular bacteria by binding to align
 N-WASP (Invasion protein) [icsA (virG)] [Shigella
 flexneri]

Score = 134 bits (338), Expect = 4e-30
 Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT---LPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVF-TWQNESNQL 453
 S I D T L +W+R + GH+ + + R Q+GG++ T + + L
 Sbjct: 806 STIVDPTTQQLSETTMWIRTVGGHNEHNLADRQLKTTANRMVYQIGGDILKTNFTDHG 865

Query: 454 SIGLMGGQAEQRSTFHNPTDNLTGKFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
 +G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F
 Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
 + + + T E+++SKGIT ++EAGY +YL PQ Q+T GV
 Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLNQVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLGSRQLQTRGVQAK--AQFSLYKNI--AIEPFAAVNALYHNKPFGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQAKGLRTSLISQSCIDKETLRKFEPPFLEVNWKSSKQYGV 1045

Query: 628 MDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRNVIELKTVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q52298 **Virulence-associated VirG [Plasmid pMYSH6000]** 1102 AA
 align

Score = 134 bits (338), Expect = 4e-30
 Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT---LPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVF-TWQNESNQL 453
 S I D T L +W+R + GH+ + + R Q+GG++ T + + L
 Sbjct: 806 STIVDPTTQQLSETTMWIRTVGGHNEHNLADRQLKTTANRMVYQIGGDILKTNFTDHG 865

Query: 454 SIGLMGGQAEQRSTFHNPTDNLTGKFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
 +G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F
 Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLPQQAQLTYLGVNGK 572
 + + + T E+++SKGIT ++EACY +YL PQ Q+T GV
 Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLNPKVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLGSRQLQTRVGQAK--AQFSLYKNI--AIEPFAAVNALYHNKPGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQAKLGLRTSLISQSCIDKETLRKFEPPFLEVNWKPSSKQYGV 1045

Query: 628 MDG-ERRVIINNKTAIESQLGVAVKIKSHLTLQATFNRQRTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRNVIELKTVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q9JMS3 YchA protein [ychA] [Escherichia coli] 1371 AA align

Score = 134 bits (337), Expect = 6e-30
 Identities = 122/461 (26%), Positives = 193/461 (41%), Gaps = 46/461 (9%)

Query: 266 DIRFNTKSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDD 322
 D+R L + +Y G D + L+ + + +G + + N
 Sbjct: 913 DLRSAAPGNILTIGGNYTGNNGTLLINTVLDSSSATDKLVIKGKDASGKTRAVTNVGGS 972

Query: 323 -LKSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEG----FLPKCKNAMIWR 376
 +L+ ++I V+G A F +G+ G Y +L + P +L KN R
 Sbjct: 973 GANTLNSIEVIHVDGNAANAEFIQAGRIAAGAYDYTLGRGPGSNYGNWYLSSKNTPEPR 1032

Query: 377 -----FMHNRLKPPPIPYCALRLNNKNSIDFDRTLPRKG-----LWL 412
 N L+P + N+ R R G +W+
 Sbjct: 1033 PDPEPTPEGHDNNLRPEASSYTANIAAANTMFVTRLHERLGQTQYVDAITGEPKATSMWM 1092

Query: 413 RVIDGHSNQWVQGK-TAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHN 470
 R GH N+W G + R +QLGG++ W +N+ +G+M G S+
 Sbjct: 1093 RHEGGH-NRWRDGSGQLKTQSNRYVIQLGGDIAQWDWGGTNRWHLGVMAGYGNHSSTGA 1151

Query: 471 PDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQRFRHRINTEDGT--ERFTS 528
 T + G+V G+ G+YATW+ + GAY D+W QY F + + DG E + S
 Sbjct: 1152 VRTGYHSKGSVNGYSTGLYATWYADDETHNGAYLDTWAQYGFWDNHVK-GDGLPGESWKS 1210

Query: 529 KGITASIEAGYNALLAEHFTKKGNSLRVYLPQQAQLTYLGVNG-KFSDSENAHVNLGSR 587
 KG+TAS+E GY + E + GN Y+QPQAQL ++GV + +S + G
 Sbjct: 1211 KGLTASLETGYAWKIGEFSSNYGNLNEWYVQPQAQLVWMGVKADELYESNGTLIESTGDG 1270

Query: 588 QLQTRVGVQA---KAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAI-E 642
 + TR+GV+ + K+ PF VN L++ + FGV M+GE + I E
 Sbjct: 1271 NVHTRLGVKTKRLNKMDDGKSREFSPFVEVNWLHNTRDFGVRMNGEPVYQDGTRNIGE 1330

Query: 643 SQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 + GV +I HL L Q G K + L +++TF
 Sbjct: 1331 VKTGVEGQINPHLNWLGNVRVQVGDKGYNDTSAMLGVKYTF 1371

tr Q6WE27 IcsA [icsA] [Shigella flexneri] 1102 AA align

Score = 134 bits (336), Expect = 7e-30
 Identities = 90/301 (29%), Positives = 150/301 (48%), Gaps = 20/301 (6%)

Query: 398 SDIFDRT---LPRKGLWLRVIDGHHSNQWVQGKTAPEGYRKGVQLGGEVF-TWQNESNQL 453
 S I D T L +W+R + GH+ + + R Q+GG++ T + + L
 Sbjct: 806 STIVDPTTQQLSETTMWIRTVGGHNEHNLADRQLKTTANRMVYQIGGDILKTNFTDHGDL 865

Query: 454 SIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSMQYQRF 513
 +G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F
 Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGTAGLYSSWFQDEKERTGLYMDAWLQYGWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLPQQAQLTYLGVNGK 572
 + + + T E+++SKGIT ++EAGY T +YL PQ Q+T GV
 Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTTHNNIDNALYLNPKVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAI-----EPFAAVNALYHNKP 623
 + + V G +Q ++G++ SL + I EPF VN + +K
 Sbjct: 986 DYIEHNGTMVTSSGVNNIQAKLGLRT---SLISHSCIDKETLRKFEPFLEVNWKWSSKQ 1041

Query: 624 FGVEMDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH-HQAKQGALNLQWT 681
 +GV M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++T
 Sbjct: 1042 YGVIMNGMSNHQIGNRNVIELKTGVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYT 1101

Query: 682 F 682
 F
 Sbjct: 1102 F 1102

tr Q8ZHA1 Putative autotransporter protein [yapH] [Yersinia pestis] 3705 AA align

Score = 130 bits (326), Expect = 1e-28
 Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDHQIIKVNGTADKHAFRLSGKHKQGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383
 ++ +G +II V G + F L+G+ G Y L Q P N + +R
 Sbjct: 3331 RTFEGIKIIDVGGDSAGQ-FTLNNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTEADDRP 3388

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHHSNQWVQGKTA 428
 P Y A N +D+F LWLR H+
 Sbjct: 3389 EPASYTANLAAANNMFTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3448

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAG 487
 + R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
 Sbjct: 3449 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSTVAQVAGYRSTGVDGYSVG 3508

Query: 488 VYATWHQLQDKQTGAYADSMQYQRFHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
 +Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
 Sbjct: 3509 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3568

Query: 547 FTKKGNSLRYLQPKQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQ-----KA 599
 + +QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
 Sbjct: 3569 VNQS-----YFIQPKAQVWVWMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3623

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
 + S A +PF N +++ K FG +DG + E +LGV ++ S L L

Subjct: 3624 KVS---GPAFKPFVEANWIHNTKDFGTLGTVKQAGTANIAELKLGVDGQVNSQLNLW 3680

Query: 659 ATFNQRTG-KHHQAKQGALNLQWTF 682

+Q G K + L +++ F

Subjct: 3681 GNIGQQVGNKGYSETSVVLGVKYNF 3705

tr Q8CZU2 Putative autotransporter adhesin [yapH] [Yersinia pestis] 3710 AA align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383

++ +G +II V G + F L+G+ G Y L Q P N + +R

Subjct: 3336 RTFEGIKIIDVGGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTEADRRP 3393

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428

P Y A N +D+F LWLR H+

Subjct: 3394 EPASYTANLAAANMFVTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3453

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDTDNLTGKVGFAG 487

+ R +QLGG+V W + L +G+M G A S+ +TG+V G+ G

Subjct: 3454 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSSTVAQVAGYRSTGSDGYSVG 3513

Query: 488 VYATWHQLQDKQTGAYADSWMQMQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546

+Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E

Subjct: 3514 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3573

Query: 547 FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQ-----KA 599

+ ++QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA

Subjct: 3574 VNQS-----YFIQPKAQVWVWGVKADDHTETNGTVISGDBGNGNIQTRLGAKAFINPSDKA 3628

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658

+ S A +PF N +++ K FG +DG + E +LGV ++ S L L

Subjct: 3629 KVS---GPAFKPFVEANWIHNTKDFGTLGTVKQAGTANIAELKLGVDGQVNSQLNLW 3685

Query: 659 ATFNQRTG-KHHQAKQGALNLQWTF 682

+Q G K + L +++ F

Subjct: 3686 GNIGQQVGNKGYSETSVVLGVKYNF 3710

tr Q9F289 YapD protein [yapD] [Yersinia pestis] 1457 AA align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383

++ +G +II V G + F L+G+ G Y L Q P N + +R

Subjct: 1083 RTFEGIKIIDVGGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTEADRRP 1140

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428

P Y A N +D+F LWLR H+

Subjct: 1141 EPASYTANLAAANMFVTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 1200

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAG 487
 + R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
 Sbjct: 1201 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSTVAQVAGYRSTGSDGYSVG 1260

Query: 488 VYATWHQLQDKQTGAYADSMQYQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
 +Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
 Sbjct: 1261 IYGSWLNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 1320

Query: 547 FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQA-----KA 599
 + +QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
 Sbjct: 1321 VNQS----YFIQPKAQVWMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 1375

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
 + S A +PF N +++ K FG +DG + E +LGV ++ S L L
 Sbjct: 1376 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 1432

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682
 +Q G K + L +++ F
 Sbjct: 1433 GNIGQQVGNKGYSETSVVLGVKYNF 1457

tr Q9F285 **YapH protein [yapH] [Yersinia pestis]** 3705 AA
align

Score = 130 bits (326), Expect = 1e-28
 Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNLK 383
 ++ +G +II V G + F L+G+ G Y L Q P N + +R
 Sbjct: 3331 RTFEGIKIIDVGGDSAGQ-FTLNRAVGGAYEYFLYQGGAS-TPDDGNWYLRTEADDRP 3388

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428
 P Y A N +D+F LWLR H+
 Sbjct: 3389 EPASYTANLAAANMFVTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDSGEL 3448

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAG 487
 + R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
 Sbjct: 3449 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSTVAQVAGYRSTGSDGYSVG 3508

Query: 488 VYATWHQLQDKQTGAYADSMQYQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
 +Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
 Sbjct: 3509 IYGSWLNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3568

Query: 547 FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQA-----KA 599
 + +QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
 Sbjct: 3569 VNQS----YFIQPKAQVWMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3623

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
 + S A +PF N +++ K FG +DG + E +LGV ++ S L L
 Sbjct: 3624 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3680

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682
 +Q G K + L +++ F
 Sbjct: 3681 GNIGQQVGNKGYSETSVVLGVKYNF 3705

tr Q74QP7 Putative autotransporter protein [yapH] [Yersinia pestis] 3710 AA align

Score = 130 bits (326), Expect = 1e-28
 Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDHQIIKVNGTADKHAFLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383
 ++ +G +II V G + F L+G+ G Y L Q P N + +R

Sbjct: 3336 RTFEGIKIIDVGGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTTEADDRP 3393

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428
 P Y A N +D+F LWLR H+

Sbjct: 3394 EPASYTANLAAANNMFVTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3453

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDTDNLLTGNVKFGAG 487
 + R +QLGG+V W + L +G+M G A S+ +TG+V G+ G

Sbjct: 3454 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVMAGYANSSSTVAQVAGYRSTGSVDGYSVG 3513

Query: 488 VYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
 +Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
 Sbjct: 3514 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3573

Query: 547 FTKKGNSLRVYLPQPAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQA-----KA 599
 + + +QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
 Sbjct: 3574 VNQS-----YFIQPKAQVWVWGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3628

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
 + S A +PF N +++ K FG +DG + E +LGV ++ S L L
 Sbjct: 3629 KVS---GPAFKPFVVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3685

Query: 659 ATFNQRTG-KHHQAKQGALNLQWTF 682
 +Q G K + L +++ F
 Sbjct: 3686 GNIGQQVGNKGYSETSVVLGVKYNF 3710

tr Q9F286 YapG protein (Putative ATP-binding transport component) 994
 (Putative AA
 autotransporter protein) [yapG] [Yersinia pestis] align

Score = 129 bits (324), Expect = 2e-28
 Identities = 84/272 (30%), Positives = 132/272 (47%), Gaps = 12/272 (4%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468
 +W+ G S + ++G VQLGG++ W NE IG++ G + +

Sbjct: 723 MWMHTQGGRSQFGHTVEQLNIKGNYYSVQLGGDIAQWATNEQGSGRIGMLAGLGKATNHS 782

Query: 469 HNPDTDNLLTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFT 527
 H+ T + G V G+ G+YATW Q TG Y D+ QY F + +N +D E++
 Sbjct: 783 HSKVTSYHSRGAVDGYNLGIYATWFADQQHNTGVYIDTLAQYSWFNNAVNGQDKAEEKYK 842

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLPQPAQLTYLGVNGK-FSDSENAHVNLGS 586
 S G T SIE+GY LA + L ++QP AQ+T+ G+N + ++ A V+ +
 Sbjct: 843 SSGFTTSIESGYTFNLA----NSDQLSYFIQPNAQITWAGINAQTHKTADGAVVSYRNN 897

Query: 587 RQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDERRVINNK--TAIESQ 644

TR+G +A Q N PF AVN ++ N+ G + G+ I+NK + E
 Sbjct: 898 GHFTRIGAKAYLQTHDTLNTKFTPVAVNWIHQNQNTGTTISGQG--IDNKIQNSTEFN 955

Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQGAL 676
 +GV +I L + A N Q G+++ AL
 Sbjct: 956 VGVESQIDQQQLHIWANINHQIGRYNYTDTNAL 987

tr Q74RV9 Putative autotransporter protein [YP2907] [Yersinia pestis] 994 AA

align

Score = 129 bits (324), Expect = 2e-28
 Identities = 84/272 (30%), Positives = 132/272 (47%), Gaps = 12/272 (4%)

Query: 410 LWLRVIDGHHSNQWVQGKTAPEVGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468
 +W+ G S + ++G VQLGG++ W NE IG++ G + +
 Sbjct: 723 MWMHTQGGRSQFGHTVEQLNIKGNYYSVQLGGDIAQWATNEQGSGRIGMLAGLGKATNHS 782

Query: 469 HNPDTDNLLTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHINTED-GTERFT 527
 H+ T + G V G+ G+YATW Q TG Y D+ QY F + +N +D E++
 Sbjct: 783 HSKVTSYHSGAVDGYNLGIYATWFADQQHNTGVYIDTLAQQYWSFNNAVNCQDKAEEKYK 842

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK-FSDSENAHVNLGS 586
 S G T SIE+GY LA + L ++QP AQ+T+ G+N + ++ A V+ +
 Sbjct: 843 SSGFTTSIESGYTFNLA----NSDQLSYFIQPNAQITWAGINAQTHKTADGAVVSYRNN 897

Query: 587 RQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNK--TAIESQ 644
 TR+G +A Q N PF AVN ++ N+ G + G+ I+NK + E
 Sbjct: 898 GHFTRIGAKAYLQTHDTLNTKFTPVAVNWIHQNQNTGTTISGQG--IDNKIQNSTEFN 955

Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQGAL 676
 +GV +I L + A N Q G+++ AL
 Sbjct: 956 VGVESQIDQQQLHIWANINHQIGRYNYTDTNAL 987

sp P77286 Hypothetical protein ydeU [ydeU] [Escherichia coli] 466 AA
YDEU_ECOLI align

Score = 129 bits (323), Expect = 2e-28
 Identities = 87/323 (26%), Positives = 155/323 (47%), Gaps = 23/323 (7%)

Query: 371 NAMIWRFMHNRALKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHHSNQWVQGKTAPV 430
 N++ +H+RL P + +D +W+R + GH
 Sbjct: 156 NSLFSHRLHDRLGEP-----QYTDSLHSQGSASSMWMRHHGHERSAGDGQLNT 205

Query: 431 EGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265

Query: 490 ATWHQLQDKQTGAYADSWMQYQRFRHINTED-GTERFTSKGITASIEAGYNALLAEHT 548
 ATW+Q +TGAY DSW Y F + +++++ + + S+G+TAS+E GY
 Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDNSVSSDNRSADDYDSRGVTASVEGGYTFEAGTFSG 325

Query: 549 KKGNNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSRQLQTRVGVQ---AKAQFSL 603

+G Y+QPQAQ+T++GV + + + + G +QTR+GV+ + Q
 Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKDSDHTRKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPGVEMDGE---RRVINNKTAIESQLGVAVKIKSHLTLQAT 660
 K +P+ N + ++K + V+M+G+ R N E + GV K+ ++L+L
 Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVGREGARNLG--EVRTGVEAKVNNNLSLWGN 443

Query: 661 FNRQTG-KHHQAKQGALNLQWTF 682
 Q G K + QG L ++++++
 Sbjct: 444 VGVQLGDKGYSQMLGVKYSW 466

tr Q8XAY3 Putative ATP-binding component of a transport system and 466
 adhesin AA
 protein [z2196] [Escherichia coli O157:H7] align

Score = 129 bits (323), Expect = 2e-28
 Identities = 86/321 (26%), Positives = 156/321 (47%), Gaps = 19/321 (5%)

Query: 371 NAMIWRFMHNLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
 N++ +H+RL P +L + S +W+R + GH
 Sbjct: 156 NSLFSHRLHDLGEQYTDLSLHSQDSASS-----MMMRHVGGERSSAGDGQLNT 205

Query: 431 EGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265

Query: 490 ATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEHFT 548
 ATW+Q +TGAY DSW Y F + +++++ + + S+G+TAS+E GY
 Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDSVSSDNRSADDYDSRGVTASVEGGYTFEAGTCG 325

Query: 549 KKGNSLRVYLQPQAQLTYLGV-NGKFDSENAHVNLGSRQLQTRGVQ---AKAQFSL 603
 +G Y+QPQAQ+T++GV + + + + G +QTR+GV+ + Q
 Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKDSDHTRKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPGVEMDGERVINNKTAI-ESQLGVAVKIKSHLTLQATFN 662
 K +P+ N + ++K + V+M+G+ + + E + GV K+ ++L+L
 Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVSRDGARNLGEVRTGVEAKVNNNLSLWGNV 445

Query: 663 RQTG-KHHQAKQGALNLQWTF 682
 Q G K + QG L ++++++
 Sbjct: 446 VQLGDKGYSQMLGVKYSW 466

tr Q7AE01 Putative ATP-binding component of a transport system and 466
 adhesin AA
 protein [ECs2116] [Escherichia coli O157:H7] align

Score = 129 bits (323), Expect = 2e-28
 Identities = 86/321 (26%), Positives = 156/321 (47%), Gaps = 19/321 (5%)

Query: 371 NAMIWRFMHNLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
 N++ +H+RL P +L + S +W+R + GH
 Sbjct: 156 NSLFSHRLHDLGEQYTDLSLHSQDSASS-----MMMRHVGGERSSAGDGQLNT 205

Query: 431 EGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265

Query: 490 ATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFTSKGITASIEAGYNALLAEHFT 548
 ATW+Q +TGAY DSW Y F + +++++ + + S+G+TAS+E GY
 Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDNSVSSDNRSADDYDSRGVTASVEGGYTFEAGTCG 325

Query: 549 KKGNSLRVYLQPQAQLTYLGV-NGKFSDENAHVNLGSRQLQTRGVQ---AKAQFSL 603
 +G Y+QPQAQ+T++GV + + + + G +QTR+GV+ + Q
 Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKDSDHARKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQATFN 662
 K +P+ N + ++K + V+M+G+ + + E + GV K+ ++L+L
 Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVSRDGARNLGEVRTGVEAKVNNNLSWGNVG 445

Query: 663 RQTG-KHHQAKQGALNLOWTF 682
 Q G K + QG L ++++++
 Sbjct: 446 VQLGDKGYSQMLGVKYSW 466

tr Q83LF4 **Hypothetical protein SF1157 [SF1157] [Shigella flexneri]** 773 AA align

Score = 128 bits (321), Expect = 4e-28
 Identities = 139/563 (24%), Positives = 231/563 (40%), Gaps = 85/563 (15%)

Query: 174 LGPKIKNSHINSEILSVGNYTEWANQVIH-----IENYVSFAAHLYSGLDPFH 224
 L I +ILS G+ AN++++H ++ VS AA ++ H
 Sbjct: 199 LESSINGQEATVDILS-GSSLRSANEILYHKDETSNVTITDSEVSSAADVFINNIKGHL 257

Query: 225 EVTDNSHVIGQT-ISLDEFR-----LENSLWEPRWDSNVGKLKTTNADIRFN-----T 271
 NS + G IS D+ +NS W+ + DS V L N+ + +
 Sbjct: 258 VDATNSKITGSANISTDDNTHTYLSLSDNSTWDIKADSTVSNLTVDNSTVYISRADGRDV 317

Query: 272 KSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDD-LKSLD 327
 + L + E+Y G R D + ++ N +GT+ + N +L+
 Sbjct: 318 EPTRLTITENYVGNNGVLHLRTELDDDSATDKVINGNTSGTTRVKVTNAGGSGAYTLN 377

Query: 328 GHQIIKVNGTAD---KHAFRLSGKHQ-----KGIYTLSLQQRPEGFLPKCKN 371
 G +II V G ++ K + +G ++ K Y + Q G +
 Sbjct: 378 GIEIISVEGESNGEFIKDSRIFAGAYEYSLTRGNTEATNKNWYLTNFQATSGGETNSGGS 437

Query: 372 AMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKG-----LWLRVI 415
 + L+P L N+ R R G LWLR I
 Sbjct: 438 SAPTVAPTPVLRPEAGSYVANLAAANTLFVMRLNDRAGEMRYIDPVTEQERSSRLWLRQI 497

Query: 416 DGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTD 474
 GH+ +R QLGG++ T +S+ +G+M G A + H+ +D
 Sbjct: 498 GGHNAWRDSNGQLRTTSHRYVSQQLGGDLTGGFTDSWRLGVMAGYARDYNLTHSSVSD 557

Query: 475 NLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFTSKGITA 533
 + G+V+G+ AG+YATW + GAY DSW QY F++ + ++ E +++KG T
 Sbjct: 558 YRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNSVKGDELAYESYAKGATV 617

Query: 534 STEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDENAHVNLGSR----- 587

S+EAGY L + F + QPQAQ ++GV+ NAH GSR
 Sbjct: 618 SLEAGYGFALNKSFGLEAAKYTWIFQPQAQAIWMGVD-----HNAHTEANGSRIENDAN 671

 Query: 588 -QLQTRVG---VQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDG---ERRVINN-- 637
 +QTR+G ++ + + S EPF +N +++++K F V M+G E+ ++N
 Sbjct: 672 NNIQTRLGFRTFIRTQEKNNSGPHGDDFEPFVEMNWIHNSKDFAVSMNGVKVEQDGVSNLG 731

 Query: 638 --KTAIESQLGVAVKIKSHLTLQ 658
 K + L A + ++ +Q
 Sbjct: 732 EIKLGVNGNLPAAASVWGNVGVQ 754

tr Q7UCU4 *Hypothetical protein [S1242] [Shigella flexneri]* 773 AA
align

Score = 128 bits (321), Expect = 4e-28
 Identities = 139/563 (24%), Positives = 231/563 (40%), Gaps = 85/563 (15%)

Query: 174 LGPKIKNSHINSEILSVGNYTEWANQVIH-----IENYVSFAAHLYSGLDPHYI 224
 L I +ILS G+ AN+,++H ++ VS AA ++ H
 Sbjct: 199 LESSINGQEATVDILS-GSSLRSANEILYHKDETSNVTITDSEVSSAADVFINNIKGHLT 257

Query: 225 EVTDNSHVIGQT-ISLDEFR-----LENSLWEPRWDSNVGKLKTTNADIRFN-----T 271
 NS + G IS D+ +NS W+ + DS V L N+ + +
 Sbjct: 258 VDATNSKITGSANISTDDNTHTYLSLDNSTWDIKADSTVSNLTVNDNSTVYISRADGRDV 317

Query: 272 KSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSIIFENPIDD-LKSLD 327
 + L + E+Y G R D + ++ N +GT+ + N +L+
 Sbjct: 318 EPTRLTITENYVGNNGVHLHRTTELDDNSATDKVINGNTSGTTRVKVTNAGGSGAYTLN 377

Query: 328 GHQIIKVNGTAD---KHAFLSGKHQ-----KGIYTLSLQQRPEGFLPKCKN 371
 G +II V G ++ K + +G ++ K Y + Q G +
 Sbjct: 378 GIEIISVEGESNGEFIKDSRIFAGAYEYSLTRGNTEATNKNWYLTNFQATSGGETNSGGS 437

Query: 372 AMIWRFMHNRLLKPIPYCALRNNKNSDIFDRTLPRKG-----LWLRVI 415
 + L+P L N+ R R G LWLR I
 Sbjct: 438 SAPTVAPTPVLRPEAGSYVANLAAANTLFVMRLNDRAGETRYIDPVTEQERSSRLWLRQI 497

Query: 416 DGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTD 474
 GH+ +R QLGG++ T +S+ +G+M G A + H+ +D
 Sbjct: 498 GGHNAWRDSNGQLRTTSHRYVSQLGGDLLTGGFTSDSWRLGVMAGYARDYNLTHSSVSD 557

Query: 475 NLTTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTERFTSKGITA 533
 + G+V+G+ AG+YATW + GAY DSW QY F++ + ++ E +++KG T
 Sbjct: 558 YRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNSVKGDELAYESYSAKGATV 617

Query: 534 SIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDENAHVNLGSR----- 587
 S+EAGY L + F + QPQAQ ++GV+ NAH GSR
 Sbjct: 618 SLEAGYGFALNKSFGLEAAKYTWIFQPQAQAIWMGVD-----HNAHTEANGSRIENDAN 671

Query: 588 -QLQTRVG---VQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDG---ERRVINN-- 637
 +QTR+G ++ + + S EPF +N +++++K F V M+G E+ ++N
 Sbjct: 672 NNIQTRLGFRTFIRTQEKNNSGPHGDDFEPFVEMNWIHNSKDFAVSMNGVKVEQDGVSNLG 731

Query: 638 --KTAIESQLGVAVKIKSHLTLQ 658
 K + L A + ++ +Q

Subjct: 732 EIKLGVNGNLNPAASVWGNVGVQ 754

tr Q9CKA8 Hypothetical protein PM1717 [PM1717] [Pasteurella multocida] 850 AA

align

Score = 126 bits (317), Expect = 1e-27
 Identities = 117/434 (26%), Positives = 199/434 (44%), Gaps = 47/434 (10%)

Query: 274 ESLLVKEDYAG-----GARFRFAYDPKEAKNTALIFEKNVTGTSIDIIFEN-PIDDLKS 325
 + + + + EDY G A F +P + L N TG + + + D +

Subjct: 429 KNVTINEDYQGHNGTLHLSADFNGTTNPTDT---LFIRGNATGKTRVAIHHIGADAENA 484

Query: 326 LDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPE-----GFLPKCKNAM 373
 + +G +II+ N + D +AF + KG + L++R E G P + M

Subjct: 485 VNGVKIIETNTSTD-NAFVIDNYLSKGAFVYHLEKRHETNQDNWYLT SYIGGTPSYRAEM 543

Query: 374 IWRFMHNRLLKPPIPYCALRLNNKNS-DIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEG 432
 N L LRL ++ S F K W+R ++G ++ ++ +

Subjct: 544 A--SYANNLYAAHQLFQLRLEDRLSRHHFLNQSADKTFWIRAVEGTNHNRMRDNQNTTKA 601

Query: 433 YRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATW 492
 R QLG V N+++ + G+M G A+Q S + + G V+G+ GVY TW

Subjct: 602 QRYVTQLGKTVI---NQAHYHA-GVMFGYAKQSSKTRSSRVGT-SRGKVQGYALGVYGTW 656

Query: 493 HQLQDKQTGAYADSWMQYQRFRHR-INTEDGTERFTSKGITASIEAGYNALLAEHFTKKG 551
 +Q + TG Y DSW+QYQ F+++ IN ++ + ++G++AS+E GY+ L + +T

Subjct: 657 YQNPNDTGLYIDSWLQYQWFKNQVINPASSSDNYRTQGLSASLELGYHLPLVQ-YTVAD 715

Query: 552 NSLRVYLPQPAQLTYLGVNGK-FSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIA-- 608
 + +QPQAQ + +N K D + ++ +G + QTR+GV +FSL +

Subjct: 716 LKHSLNIPQPAQFIWQKLN SKQHRDPQQTLIHYIGQQNTQTRLGV---RFSLDSHFLNT 771

Query: 609 ---IEPFAAVNALYHNKPGVEM-DGERRVINNKTAIESQLGAVVKIKSHLTLQATFNRQ 664
 ++P+ VN L+H K +G+ + D + K E + G+A + HL Q

Subjct: 772 QWNLKPYFEVNWLHHAKDYGITINDVVNHIEGAKQLFEYKAGIASQFGRHLRFWLDTTHQ 831

Query: 665 TGKHHQAKQGALNL 678

GK Q K LN+

Subjct: 832 RGK-QQFKDNQLNV 844

tr P75997 Putative part of putative ATP-binding component of a transport system [b1170] [Escherichia coli K12] 338 AA

align

Score = 118 bits (296), Expect = 3e-25
 Identities = 76/234 (32%), Positives = 119/234 (50%), Gaps = 19/234 (8%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468
 LWLR I GH+ +R QLGG++ T +S+ +G+M G A +

Subjct: 66 LWLRQIGGHHNAWRDSNGQLRTTSHRYVSQLGGDLLTGGFTDSDSWRLGVMAGYARDYNLT 125

Query: 469 HNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHINTED-GTERFT 527

H+ +D + G+V+G+ AG+YATW + GAY DSW QY F++ + ++ E ++
 Sbjct: 126 HSSVSDYRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNVKGDELAYESYS 185

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNGKFSDSENAHVNLGSR 587
 +KG T S+EAGY L + F + QPOAQ ++GV+ NAH GSR
 Sbjct: 186 AKGATVSLEAGYGFALNKSFGLEAAKYTWIFQPQAOQAIWMGVD-----HNAHTEANGSR 239

Query: 588 -----QLQTRVG---VQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDG 630
 +QTR+G ++ + + S EPF +N +++++K F V M+G
 Sbjct: 240 IENDANNNIQTRLGFRTFIRTQEKNNSGPHGDDFEPFVEMNWIHNSKDFAVSMNG 293

sp Q03155 Adhesin aidA-I precursor [aidA-I] [Escherichia coli] 1286 AA
 AIDA_ECOLI align

Score = 118 bits (295), Expect = 4e-25
 Identities = 105/414 (25%), Positives = 186/414 (44%), Gaps = 40/414 (9%)

Query: 302 LIFEKNVTGTSIDIIFENPIDDL-KSLDGHQIIVNGTADKHAFRLSGKHQKGIYTLSSLQQ 360
 L+ + N +G SDI++ N ++ DG II V G +D F L + G Y +LQ+
 Sbjct: 880 LVVKGNNTSGQSDIVYVNEDGSGGQTRDGINIISVEGNSDAE-FSLKNRVVAGAYDYTLQK 938

Query: 361 RPEGFLPKCKNAMIWRFMH-----NRLKPPIPYCALRLNNKNS-----DIF 401
 E N + H + +P A + NS +
 Sbjct: 939 GNES---GTDNKGWYLTSHLPTSDTRQYRPENGSYATNMALANSFLMDLNERKQFRAMS 995

Query: 402 DRTLPRKG-LWLRVIDGHSNQWV---QGKTAPVEGYRKGVQLGGEVFTWQNES-NQLSIG 456
 D T P +W+++ G S+ + Q KT + QLGG+++ + E ++G
 Sbjct: 996 DNTQPESASVWMKITGGISSLNGQNKTTTNQFIN---QLGGDIYKFHAEQLGDFTLG 1052

Query: 457 LMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHR 516
 +MGG A + N ++ + G+ GVY TW+Q + TG +A++WMQY F
 Sbjct: 1053 IMGGYANAKGKTINYTSNKAARNTLDGYSVGVYGTWYQNGENATGLFAETWMQYNWFNAS 1112

Query: 517 INTED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAOQLTYLGVNGKFSD 575
 + + E++ G+TAS GYN + + +G + +LQP Q ++GV
 Sbjct: 1113 VKGDGLEEEKYNLNGLTASAGGGYNLNVHTWTSPEGITGEFWLQPHLQAVWMGVTPDTHQ 1172

Query: 576 SENAHL-VNLLGSRQLQTRGVQAA-KAQFSLYKNIA-IEPFAAVNALYHNKPGVEMDG 630
 +N V G +QT+ G+A K + +L K+ P+ N +++ FGV+M
 Sbjct: 1173 EDNGTUVQGAGKNNIQTAKAGIRASWKVKSTLDKTGRFRPYIEANWIHNTHEFGVKMSD 1232

Query: 631 ERRVIN-NKTAIESQLGAVKIKSHLTLQATFNRQTGKH-HQAKQGALNLQWTF 682
 + +++++ ++ E + G+ I +L++ Q G H A GAL +++++F
 Sbjct: 1233 DSQQLSGSRNQGEIKTGIEGVITQNLNVNGGVAYQAGGHGSNAISGALGIKYSF 1286

tr Q7CPG9 Putative autotransported protein [misL] [Salmonella typhimurium] 955
 AA align

Score = 110 bits (276), Expect = 7e-23
 Identities = 81/286 (28%), Positives = 142/286 (49%), Gaps = 22/286 (7%)

Query: 410 LWLRVIDGHS--NQWVQGKTAPVEGYRKGVQLGGEVFTWQNES-NQLSIGLMGGQAEQRS 466

LW+R + H+ N + Y +QLGG++ W + ++ IG M G A ++
 Sbjct: 679 LWMRNVAHTRFNDGSGQLKTRINSYV--LQLGGDLAQWSTDGLDRWHIGAMAGYANSQN 736

Query: 467 TFHNPDTDNLLTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTER 525
 + +D + G V G+ G+Y TW+ ++GAY D+WM Y F +++ +D E+
 Sbjct: 737 RTLSSVSDYHSRGQVTGYSVGLYGTWYANNIDRSGAYVDTWMLYNWFDNKVMGQDQAAEK 796

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGVNGKFSDENAHVNL- 584
 + SKGITAS+EAGY+ L E + +LQP+AQ+ ++GV D+ A+ L+
 Sbjct: 797 YKSKGITASVEAGYSFRLGESAHQS----YWLQPKAQVVMGVQA--DDNREANGTLVK 849

Query: 585 --GSRQLQTRGVQAKAQ----FSLYKNIAIEPFAAVNALYHNKPGVEMDG-ERRVIINN 637
 + L TR+GV+A K+ +PF N +++ +P V+MD +
 Sbjct: 850 DDTAGNLLTRMGVKAYINGHNAIDNDKSREFQPFVEANWIHNTQPASVKMDDVSSDMRGT 909

Query: 638 KTAIESQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 K E ++G+ ++ L + +Q G + QG L ++++F
 Sbjct: 910 KNIGELKVGIEGQVTPRLNVWGNVAQQVGDGTGYSQGMLGMKYSF 955

tr Q9Z625 MisL [misL] [Salmonella typhimurium] 955 AA
align

Score = 110 bits (276), Expect = 7e-23
 Identities = 81/286 (28%), Positives = 142/286 (49%), Gaps = 22/286 (7%)

Query: 410 LWLRVIDGHS--NQWVQGKTAPVEGYRKGVQLGGEVFTWQNES-NQLSIGLMGGQAEQRS 466
 LW+R + H+ N + Y +QLGG++ W + ++ IG M G A ++
 Sbjct: 679 LWMRNVAHTRFNDGSGQLKTRINSYV--LQLGGDLAQWSTDGLDRWHIGAMAGYANSQN 736

Query: 467 TFHNPDTDNLLTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED-GTER 525
 + +D + G V G+ G+Y TW+ ++GAY D+WM Y F +++ +D E+
 Sbjct: 737 RTLSSVSDYHSRGQVTGYSVGLYGTWYANNIDRSGAYVDTWMLYNWFDNKVMGQDQAAEK 796

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGVNGKFSDENAHVNL- 584
 + SKGITAS+EAGY+ L E + +LQP+AQ+ ++GV D+ A+ L+
 Sbjct: 797 YKSKGITASVEAGYSFRLGESAHQS----YWLQPKAQVVMGVQA--DDNREANGTLVK 849

Query: 585 --GSRQLQTRGVQAKAQ----FSLYKNIAIEPFAAVNALYHNKPGVEMDG-ERRVIINN 637
 + L TR+GV+A K+ +PF N +++ +P V+MD +
 Sbjct: 850 DDTAGNLLTRMGVKAYINGHNAIDNDKSREFQPFVEANWIHNTQPASVKMDDVSSDMRGT 909

Query: 638 KTAIESQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 K E ++G+ ++ L + +Q G + QG L ++++F
 Sbjct: 910 KNIGELKVGIEGQVTPRLNVWGNVAQQVGDGTGYSQGMLGMKYSF 955

sp P45508 Hypothetical protein yfaL precursor [yfaL] [Escherichia 1250
 YFAL_ECOLI coli] AA
align

Score = 96.3 bits (238), Expect = 2e-18
 Identities = 74/279 (26%), Positives = 136/279 (48%), Gaps = 27/279 (9%)

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469

Query: 470 NPDTDNLTGKVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRIN-TEDGTERFTS 528
 Sbjct: 989 LRVIGG DYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSR 1046

Query: 529 KGITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGV-NGKFSDENAHVNLGSR 587
 Sbjct: 1047 SNMTGTRADNQNHG YAVGLTSSWFQHGNQKQGAWLDSWLQYAWFSNDVSEQEDGTDHYHS 1106

Query: 588 QLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINN---KTAIESQ 644
 Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYYHDPHSTEIEEDGSTISDDAVKQRGEIK 1211

Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
 Sbjct: 1212 VGVTGNISQRVSLRGSVAWQKGSDDFAQTAGFLSMTVKW 1250

tr Q8ZN57 Similar to the C-terminal region of AIDA [shdA] [Salmonella 2039 AA typhimurium]

align

Score = 95.5 bits (236), Expect = 3e-18
 Identities = 75/289 (25%), Positives = 128/289 (43%), Gaps = 29/289 (10%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
 Sbjct: 1764 VWARFKAGKAESAEAVSGNIDMDSNSYQFOLGGDILAWNGQQSVTVGVM-----ASYI 1816

Query: 470 NPDTDNL-----TTGKVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRIN 518
 Sbjct: 1817 NADTDSTGNRGADGSQFTSSGNVDGYNLGVYATWFADAQTHSGAYVDSWYQYGFYNSVE 1876

Query: 519 TED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGVNG-KFSDS 576
 Sbjct: 1877 SGDAGSESYDSTANAVSLETGYRYDIA---LSNGNT--VSLTPQAQVWQNYSAKSVKD 1931

Query: 577 ENAHVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVIN 636
 Sbjct: 1932 YGTRIDGQDGDSWTTRLGLRVDGKLYKGSRTVIQPF AEWNLHTSDDVSF-DATVKQ 1990

Query: 637 NKTA--IESQLGVAVKIKSHLTLQATFNRQTGKHHQAK-QGALNLQWTF 682
 Sbjct: 1991 DLPANRAELKVGLQADIDKQWSVRAQVAGQTGSNDFGDLNGSLNLRYNW 2039

tr Q8CVV7 Hypothetical protein yfaL [yfaL] [Escherichia coli 1254 AA 06]

Score = 95.5 bits (236), Expect = 3e-18
 Identities = 71/278 (25%), Positives = 138/278 (49%), Gaps = 25/278 (8%)

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFH 470

Sbjct: 993 LRVIGGRYHYTAVGQLAQHED-TSTVQLSGNLFSGHWGDDGEWMLGIVGGYSDNQGDSRS 1051
 Query: 471 PDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRIN-TEDGTERFTSK 529
 Sbjct: 1052 NMTGTRADNQNQHGYAVGLTSSWYQHGNQKQGAWLDSWLQYAWFNNDVSEQDDGVDHYHSS 1111
 Query: 530 GITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGV-NGKFSDENAHVNLGSRQ 588
 Sbjct: 1112 GIIASLEAGYQWLPGR-----GVVIEPQAQVIYQGVQQDDFTAANHARVSQSQGDD 1162
 Query: 589 LQTRGVGQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINKTAI---ESQL 645
 Sbjct: 1163 IQTRLGLHSEWRTA---VSVTPTLDLN--YYHDPHATEIEEDGSTISDDAAKQRGEIKV 1216
 Query: 646 GVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
 Sbjct: 1217 GITGNISQRVSLRGSAWQKGSDDFAQTAGFLSMTVKW 1254

tr Q9XCJ4 ShdA [shdA] [Salmonella typhimurium] 2035 AA
align

Score = 95.5 bits (236), Expect = 3e-18
 Identities = 75/289 (25%), Positives = 128/289 (43%), Gaps = 29/289 (10%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
 Sbjct: 1760 VWARFKAGKAESEAVSGNIDMDSNYSQFQLGGDILAWGNGQQSVTVGVM-----ASYI 1812

Query: 470 NPDTDNL-----TTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRIN 518
 Sbjct: 1813 NADTDSTGNRGADGSQFTSSGNVDGYNLGVYATWFADAQTHSGAYVDSWYQYGFYNNNSVE 1872

Query: 519 TED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQACLTYLGVNG-KFSDS 576
 Sbjct: 1873 SGDAGSESYDSTANAVSLETGYRYDIA---LSNGNT--VSLTPQAQVWQNYSAHSVKD 1927

Query: 577 ENAHVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVIN 636
 Sbjct: 1928 YGTRIDGQDGDSWTRRLGLRVDGKLYKGSRTVIQPFAEANWLHTSDDVSVD-FATVKQ 1986

Query: 637 NKTA--IESQLGVAVKIKSHLTLQATFNRQTGKHHQAK-QGALNLQWTF 682
 Sbjct: 1987 DL PANRAELKVGLQADIDKQWSVRAQVAGQTGSNDFGDLNGSLNLRYNW 2035

tr Q8XE28 Putative ATP-binding component of a transport system [yfaL] 1250 AA
 [Escherichia coli O157:H7]
align

Score = 93.2 bits (230), Expect = 1e-17
 Identities = 72/279 (25%), Positives = 134/279 (47%), Gaps = 27/279 (9%)

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469
 Sbjct: 989 LRVIGGYDYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSR 1046

Query: 470 NPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHPRINT-EDGTERFTS 528
 Sbjct: 1047 SSMTGTRADNQNHNHYAVGLTSSWFQHKGKQKGAWLDNLQYAWFSNDVSEHEDGVDHYHS 1106

Query: 529 KGITASIEAGYNALLAEHFTKKGNLSRVYLQPKAQQLTYLGV-NGKFSDSENAHVNLGSR 587
 Sbjct: 1107 SGIIASLEAGYQWLPGR-----GVVIEPQAQVYQGVQQDDFTAANRARVSQSQGD 1157

Query: 588 QLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINN---KTAIESQ 644
 Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYYHDPHSTEIEEDASTISDDAVKQRGEIK 1211

Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
 Sbjct: 1212 VGVTGNISQRVSLRGSAWQKGSDDFAQTAGFLSMTVKW 1250

tr Q7AC44 Putative ATP-binding component of a transport system 1250
 [ECs3116] AA
 [Escherichia coli O157:H7] align

Score = 93.2 bits (230), Expect = 1e-17
 Identities = 72/279 (25%), Positives = 134/279 (47%), Gaps = 27/279 (9%)

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469
 Sbjct: 989 LRVIGGYDYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSR 1046

Query: 470 NPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHPRINT-EDGTERFTS 528
 Sbjct: 1047 SSMTGTRADNQNHNHYAVGLTSSWFQHKGKQKGAWLDNLQYAWFSNDVSEHEDGVDHYHS 1106

Query: 529 KGITASIEAGYNALLAEHFTKKGNLSRVYLQPKAQQLTYLGV-NGKFSDSENAHVNLGSR 587
 Sbjct: 1107 SGIIASLEAGYQWLPGR-----GVVIEPQAQVYQGVQQDDFTAANRARVSQSQGD 1157

Query: 588 QLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINN---KTAIESQ 644
 Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYYHDPHSTEIEEDASTISDDAVKQRGEIK 1211

Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
 Sbjct: 1212 VGVTGNISQRVSLRGSAWQKGSDDFAQTAGFLSMTVKW 1250

tr Q9FCW0 Hypothetical protein [Kluyvera ascorbata] 652 AA
 align

Score = 73.9 bits (180), Expect = 9e-12
 Identities = 76/299 (25%), Positives = 123/299 (40%), Gaps = 44/299 (14%)

Query: 246 NSLWEPRWDSNVGKLKTTNADIRFNTKSES-LLVKEDYAGG---ARFRFAYDPKEAKNT 300

NSLW+ DS + L N + + S L V + Y G R +
 Sbjct: 361 NSLWKMTGDSVLSSLTLNNGTVEWAGASAGNVLTAVAGNYQGNGLRINTVLGDDNSVTD 420

Query: 301 ALIFEKNVTGTSIIIFENPIDDL-KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQ 359
 L+ E + +GT+ + N K+++G ++I V+G +D + F SG+ G Y +L+
 Sbjct: 421 KLVVEGDTSGTTFVAVTNAGGSGDKTINGIEVIHVDGASDGN-FVQSGRIVAGSYEYALR 479

Query: 360 QRPEGFLPKCKNAMIWRFMHNRLKP--PIP-----YCALRLNNKNSDIFDRTLP 406
 R EG W M+ P P+P Y A L N+ R
 Sbjct: 480 -RGEFTAfnH----WYLMNAATTPEEPVPEKPTLRPESGSYIA-NLAAANTMFTTRLHD 532

Query: 407 RKG-----LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NE 449
 R G +W+R + GH+ + R +QLGG++ W N
 Sbjct: 533 RLGETQYIARLTGEQKVTSWMRNVGGHTRFKDSSGQLSTQSNRYVLQLGGDIAQWSTNG 592

Query: 450 SNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVYATWHQLQDKQTGAYADSWM 508
 ++ +GLM G +S + + + G V G+ AG+Y TW+ + +TG+Y DSW+
 Sbjct: 593 LDRWHLGLMAGYGNQSNTKSDVSRYHSRGQVTGYSAGIYGTWYANEADKTGSYLDWSI 651

tr Q6IU25 YdeU (Fragment) [Escherichia coli B] 169 AA
align

Score = 70.5 bits (171), Expect = 1e-10
 Identities = 39/138 (28%), Positives = 63/138 (45%), Gaps = 11/138 (7%)

Query: 371 NAMIWRFMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
 N++ +H+RL P + +D +W+R + GH
 Sbjct: 41 NSLFSHRLHDLRLGEP-----QYTDSLHSQGSASSMWMRHVGHERSRAVDQLNT 90

Query: 431 EGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 91 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 150

Query: 490 ATWHQLQDKQTGAYADSW 507
 ATW+Q +TGAY DSW
 Sbjct: 151 ATWYQNDANKTGAYVDSW 168

tr Q88LP9 Outer membrane autotransporter [PP1880] [Pseudomonas putida
 (strain
 KT2440)] 730
AA
align

Score = 66.2 bits (160), Expect = 2e-09
 Identities = 109/474 (22%), Positives = 183/474 (37%), Gaps = 84/474 (17%)

Query: 228 DNSHVIGQTIS-----LDEF-----RLENSL-----WEPRWDSNVGKLKTTN 264
 +NSH++G ++ L+ F RL+N W +S V L N
 Sbjct: 257 NNShLVGDIVAASGGTANVLLENFATLKGRLDNVASLEINSGGEWTLVDNSQVTDLSLDN 316

Query: 265 ADIRFNTKSESLLVK-EDYAGGARFRFAYDPKEAKNTALIFEKNVTGTS-----IIFEN 318
 +RF E + E+ G F D +++ L +VTGT+ +I +
 Sbjct: 317 GAVRFGGPGEFFTLSVENLTGNGTFIMEADFSTSQSDFL---DVTGTASGNHQLLISAS 372

Query: 319 PIDDLSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEG-----FLPK 368

D L H + G D L G G Y+ L QR + P
 Sbjct: 373 GNDPLTDNSLHVHTAAG--DSQFSLLGGSVDLGAYSYDLVQRGDNDWYLDATTRTVSPG 430

Query: 369 CKNAMIWRFMHNLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKT- 427
 + M + P I Y L + R + G W+R + NQ+ T
 Sbjct: 431 TQTVMALA---NVVPTIWYGELGVLSRMRGDVRRNPGKAGGWVR---SYGNQFNVSATS 483

Query: 428 -APVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNN--VKG 483
 A + ++G+ +G + + N L +G+ G + N D NL G+ V
 Sbjct: 484 GAAYQQQQQGLSIGADAPLAAGDGNWL-VGITAG-----YSNSDL-NLARGSSASVDS 534

Query: 484 FGAGVYATWHQLQDKQTGAYADSWMXYQRFRHR--INTEDGTER---FTSKGITASIEAG 538
 + AG YATW D ++G Y D+ + RFR++ + DG++ +++ G S+E G
 Sbjct: 535 YHAGAYATW---LDPESGYYIDTVARINRFRNQADVRLSDGSKAKGDYSNLGAGVSLEVG 591

Query: 539 YNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK-FSDSENAHVNLGSRQLQTRGVQA 597
 + LA+ + +L+P AQL+ L V GK +S N + L +VG
 Sbjct: 592 RHLNLADDW-----FLEPFAQLSGLKVQGKDYSLDNGMRANSNSTHSLLGKVGT 642

Query: 598 KAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQLGVAVKI 651
 FS +--+P+ V A++ + R +N +--+G V +
 Sbjct: 643 GRTFSAGTGRSVQPYLRAVHEFVNDNQVKVNDNRFSSNLAGSRAEIGAGVAV 696

tr Q884S7 Autotransporter, putative [PSPTO2011] [Pseudomonas syringae 769
 (pv. AA
 tomato)] align

Score = 66.2 bits (160), Expect = 2e-09
 Identities = 105/460 (22%), Positives = 184/460 (39%), Gaps = 58/460 (12%)

Query: 249 WEPRWDSNVGKLKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNTALIFEKNV 308
 W+ + D+ V L + F + L + +G F D A +
 Sbjct: 342 WQMQGDNAVTSLSMQGGSGVFGGEGFHTLSNELSGSGTFGLRVLDNAVGDLINVNGQA 401

Query: 309 TGTSDIIFENPIDDLKSLDGHQIIKVNGT--ADKHAFRLSGKHQKGIYTLSLQQRPEGFL 366
 +G + N ++ S D Q +KV T D L G+ G Y+ L+Q+ +
 Sbjct: 402 SGQFGLRVRNTGVEVISAD-MQPLKVVHTEGGDAQFSLLGGRVDLGAYSYLLEQQGNDWF 460

Query: 367 PKCKNAMIWRFMHNLK----PPIPYCALR-LNNKNSDIFDRTLPRKGLWLRVIDGHSN 420
 ++ +I + L P I L L ++ ++ R + G W+R N
 Sbjct: 461 VVGRDKVISPTQSALALYSAAPAIWMSLSTLRSRMGEV--RASGQAGGWMRAYGSRLN 518

Query: 421 QWVQGKTAPVEGYRK---GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLT 477
 T+ YR+ G+ LG + + +L +G++GG + + D T
 Sbjct: 519 ---ATTSDGVDYRQKQSGLSLGADAPV-EVSNGRLLVGVLGGYSTS----DLDVSRGT 568

Query: 478 TGNVKGFGAGVYATWHQLQDKQTGAYADSWMXYQRFRHR--INTEDGTER---FTSKGIT 532
 TG V + AG Y TW L D G Y D ++ RFR++ + D ++ +++ G+
 Sbjct: 569 TGKVASYYAGAYGTW--LSD--DGYYVDGVLKLNFRNKAADVAMSASKAKGDYSNTGVG 624

Query: 533 ASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSSENADHVNLGSRQLQTR 592
 +EAG + LA+ + +L+P AQL+ + V G+ +N + ++ +TR
 Sbjct: 625 GWVEAGRHIKLADDY-----FLEPFAQLSSVVQGQELLDNG---MKAKNARTR 671

Query: 593 VGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQL----- 645

V K SL + +A++ V Y E V N ++ L
 Sbjct: 672 -SVLGKVGTSLGRTVALKD-GGVLQPYVRVAVAQEFSRRNEVKANDVKFDNSLFGSRGEL 729

Query: 646 --GVAVKIKSHLTLQATFNRQTGKHHQAKQGA-LNLQWTF 682

GV+V + L L A + G+H + GA + L+ TF
 Sbjct: 730 GAGVSVSLSERLKLHADVDYMKGQHIEQPWGANVGLRLTF 769

tr Q7VYJ2 Autotransporter [BP1344] [Bordetella pertussis] 866 AA
align

Score = 65.5 bits (158), Expect = 3e-09

Identities = 79/308 (25%), Positives = 131/308 (41%), Gaps = 46/308 (14%)

Query: 397 NSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTW-QNESNQLS 454
 N + R R W R G+S Q + G P ++ GVQLG +++++ + + Q

Sbjct: 583 NQALLARDGERVAAWARAYGGNSKQALDGDAQPGIDARLAGVQLGQDLYSSVRPDGGQHR 642

Query: 455 IGLMGGQAEQRSTFHNP--DTDNLTG -VKGFGAGVYATWHQLQDKQTGAY-ADSWMQ 509
 GL GG + R H + TG + G+ G Y T+ + A A++WM

Sbjct: 643 FGLFGGGYQARGDTHGSAGGERDAATGRLTIDGYSVGGYWTYVGPRGWYDAVLANTWMD 702

Query: 510 YQRFRHrintEDGTERFT-SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTY-- 566
 +++ G + T + TAS+E+GY L+E +T L+PQAQL Y

Sbjct: 703 IDT----DSKAGRDACTRQQAFTASLESGYPLALSERWT-----LEPQAQLIYQH 748

Query: 567 LGVNGKFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGV 626
 V+G FSD+ + V + L R+G + + +++ + P+AA+N F

Sbjct: 749 TRVDG-FSDAV-SEVRIRDDNALTARLGARLQGEYAAAQV-WRPYAAALN-----FWR 798

Query: 627 EMDGERRVI-----NNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGA-- 675
 GE V+ T++E G +V + L L T Q +GA

Sbjct: 799 TFSGENTVVLGEDSIDTRRGATSLELAAGASVTLARSLALYGRAYATSIDSQYLRGASA 858

Query: 676 -LNLQWTF 682
 L + + + T+

Sbjct: 859 QLGMRYTW 866

tr Q7WIM1 Putative autotransporter [BB2830] [Bordetella bronchiseptica] 849 AA
 (Alcaligenes bronchisepticus)]

align

Score = 64.3 bits (155), Expect = 7e-09

Identities = 75/304 (24%), Positives = 125/304 (40%), Gaps = 38/304 (12%)

Query: 397 NSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTW-QNESNQLS 454
 N + R R W R G+S Q + G P ++ GVQLG +++++ + + Q

Sbjct: 566 NQALLARDGERVAAWARAYGGNSKQALDGDAQPGIDARLAGVQLGQDLYSSVRPDGGQHR 625

Query: 455 IGLMGGQAEQRSTFHNP--DTDNLTG -VKGFGAGVYATWHQLQDKQTGAYADSWMQYQR 512
 GL GG R H + TG + G V W + + G Y D+ +

Sbjct: 626 FGLFGGGYGHARGDTHGSAGGERDAATGRLTIDGYSVGGYWTYVGPR--GWYVDTVLANTW 683

Query: 513 FRHRINTEDGTERFT-SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN- 570

+++ G + T + +TAS+E+GY L+E +T L+PQAQL Y
 Sbjct: 684 MDIDTDSKAGRDACTRQQLALTASLESGYPLALSERWT-----LEPQAQLIYQHTRV 734

Query: 571 GKFSDENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDG 630
 FSD+ + V + L R+G + + +++ + P+AA+N F G
 Sbjct: 735 DDFSDAV-SEVRIRDDNALTARLGARLQGEYAAAQV-WRPyAALN-----FWRTFSG 785

Query: 631 ERRVI-----NNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGA---LNL 678
 E V+ T+E G +V+ L L T Q +GA L +
 Sbjct: 786 ENTVVLGEDSIDTRRGATSLELAAGASVTLARSLALYGRAYATSIDSQYLRGASAQLGM 845

Query: 679 QWTF 682
 ++T+
 Sbjct: 846 RYT W 849

tr Q883X2 Autotransporter, putative [PSPT02225] [Pseudomonas syringae] 773
 (pv.
 tomato)] AA align

Score = 63.9 bits (154), Expect = 9e-09
 Identities = 69/283 (24%), Positives = 116/283 (40%), Gaps = 39/283 (13%)

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRK---GVQLGGEVFTWQNESNQLSIGLMGGQAE 463
 + G W+R N A GY++ G LG + + L+ G+M GQ+
 Sbjct: 508 QSGAWMRTYGNKFNV---SDASGFGYQQTQQGFSLGADGKVPMDGQWLA-GVMAGQSS 562

Query: 464 QRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRH--RINTED 521
 + D +G V + G Y+TW D TG Y D +++ RF + R+N D
 Sbjct: 563 SDLSL----DRGASGKVDSYVGAYSTW---LSDTGYYFDGVLKFNRFNNKARVNLS 614

Query: 522 GTER---FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSSEN 578
 GT +++ G+ AS+E G + L + +++P +QL + V GK + +N
 Sbjct: 615 GTRTKGDYSNSGVGASLEFGRHIKLDNGY-----FVEPYSQLAGVVVEGKDYELDN 665

Query: 579 ---AHVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVI 635
 A +L +R L ++G F L + ++P+ A H E+ V
 Sbjct: 666 GMRAENDL--TRSLVGKLGATTGRNFDLGQGRTVQPYVR-TAWVHEFAKNNEVQVNDNVF 722

Query: 636 NNK---TAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGA 675
 NN + E +G+A + + A F G + GA
 Sbjct: 723 NNDLSGSRGELGIGIAASLSERFQVHADFEHSNGDKVEQPWGA 765

tr Q7WIB0 Putative autotransporter [BB2941] [Bordetella bronchiseptica] 937 AA
 (Alcaligenes bronchisepticus)] align

Score = 55.5 bits (132), Expect = 3e-06
 Identities = 106/493 (21%), Positives = 170/493 (33%), Gaps = 76/493 (15%)

Query: 224 IEVTDNSHVIGQTISLDEFRL-ENSLWEPRWDSNVGKLKTT-NADIRFNTKSE---SLLV 278
 ++V D + G T SLD L W S+VG+L A + F + L
 Sbjct: 477 LDVADGAQWHGATQSLDRLALGAGGQWRMSAASSVGELSMEPGAAVFGDAAGPGFQTLT 536

Query: 279 KEDYAGGARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDDLKSLDGHQIIKVNGTA 338
 AG F D L+ G + P S Q + V A
 Sbjct: 537 VRTLHAGAGSFEMRADAALAHADQLVVTDQAEGRHRVWLRAPAGAEPSKA--QAVLVRAPA 594

Query: 339 D-KHAFRLSGKHQK---GIYTLSLQQRPEGFLPKCKNAM-----IWR 376
 D K +F L G + G Y L Q+P G + +W
 Sbjct: 595 DGKASFELDGSDFGRADFGTYRYGLAQQPGGAWGLVRTGYSSTAAAALDTGGLGAVQGLWY 654

Query: 377 FMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRK 436
 N L + LRLN + R ++ R+ + QG + G
 Sbjct: 655 AESNALGKRMG--ELRLNPDAGGAWGRAFSQRQ--RISPRAGRHFQQGVS-----G 701

Query: 437 VQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQ 496
 ++LG + W + G + G F + + +V G+ + A
 Sbjct: 702 IELGADR-AWPVAGGRWHAGGLLGYTRASRGFSGQGKHTDSVHVGYYATYIGAN---- 755

Query: 497 DKQTGAYADSMQYQRFRHRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKK 551
 G YAD+ ++ RF + + R + + G+ ++EAG L H+
 Sbjct: 756 ----GVYADATLRAFENSFDVPGWAGRTVSGSYRANGVGTLEAGRRALDRHW---- 807

Query: 552 NSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIE 610
 + + + PQA+L + G ++ S + G LQ RVG QA +F L + +
 Sbjct: 808 ----FVEPQAEALAWFRAGGGTYTASNGLRIEDDGGTSLQARVGAQAGRRFDLRRGAVVQ 862

Query: 611 PFAAVNALYHNKPGF-VEMDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH 668
 P+A ++ + K V +G R +E LGVA + L A++ G
 Sbjct: 863 PYAQLSWVQELKGVSTVRTNGIAHRTDLGAGRVELGLVAAALGKGNLYASYEYAHGPR 922

Query: 669 HQAKQGALNLQWT 681
 L+L WT
 Sbjct: 923 -----LSLPWT 928

tr Q7W6E1 Putative autotransporter [BPP2975] [Bordetella parapertussis] 937 AA

align

Score = 55.5 bits (132), Expect = 3e-06
 Identities = 106/493 (21%), Positives = 170/493 (33%), Gaps = 76/493 (15%)

Query: 224 IEVTDNSHVIGQTISLDEFRL-ENSLWEPRWDSNVGKLKTT-NADIRFNTKSE---SLLV 278
 ++V D + G T SLD L W S+VG+L A + F + L
 Sbjct: 477 LDVADGAQWHGATQSLDRLALGAGGQWRMSAASSVGELSMEPGAAVVFGDAAGPGFQTLT 536

Query: 279 KEDYAGGARFRFAYDPKEAKNTALIFEKNVTGTSIIIFENPIDDLKSLDGHQIIKVNGTA 338
 AG F D L+ G + P S Q + V A
 Sbjct: 537 VRTLHAGAGSFEMRADAALAHADQLVVTDQAEGRHRVWLRAPAGAEPSKA--QAVLVRAPA 594

Query: 339 D-KHAFRLSGKHQK---GIYTLSLQQRPEGFLPKCKNAM-----IWR 376
 D K +F L G + G Y L Q+P G + +W
 Sbjct: 595 DGKASFELDGSDFGRADFGTYRYGLAQQPGGAWGLVRTGYSSTAAAALDTGGLGAVQGLWY 654

Query: 377 FMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRK 436
 N L + LRLN + R ++ R+ + QG + G
 Sbjct: 655 AESNALGKRMG--ELRLNPDAGGAWGRAFSQRQ--RISPRAGRHFQQGVS-----G 701

Query: 437 VQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLLTGNVKFGAGVYATWHQLQ 496
 +LG + W + G + G F + + +V G+ + A
 Sbjct: 702 IELGADR-AWPVAGGRWHAGGLLGYTRASRGFSGQGKHTDSVHVGYYATYIGAN----- 755

Query: 497 DKQTGAYADSWMQMQRFRHINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKG 551
 G YAD+ ++ RF + + R + + G+ ++EAG L H+
 Sbjct: 756 -----GVYADATLRAZRFEFDVPGWAGRTVSGSYRANGVGTLEAGRRLALDRHW---- 807

Query: 552 NSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVVQAKAQFSLYKNIAIE 610
 +++PQA+L + G ++ S + G LQ RVG QA +F L ++
 Sbjct: 808 -----FVEPQAEELAWFRAGGGTYTASNGLRIEDDGTSIQLARVGAQAGRRFDLRGGAVVQ 862

Query: 611 PFAAVNALYHNKPGF-VEMDG-ERRVINNKTAIESQLGVAVKIKSHLTQATFNRQTGKH 668
 P+A ++ + K V +G R +E LGVA + L A++ G
 Sbjct: 863 PYAQLSWVQELKGVSTVRTNGIAHRTDLGAGRVELGLGVAAALGKGNLYASYEYAHGPR 922

Query: 669 HQAKQGALNLQWT 681
 L+L WT
 Sbjct: 923 -----LSLPWT 928

tr Q7WQ80 Autotransporter [BB0452] [Bordetella bronchiseptica] 2377
 (Alcaligenes AA
 bronchisepticus) align

Score = 53.9 bits (128), Expect = 1e-05
 Identities = 58/257 (22%), Positives = 103/257 (39%), Gaps = 29/257 (11%)

Query: 408 KGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQR 465
 +G W R + G+ AP +G+ G QLG +++ + + + G+ GG A R
 Sbjct: 2103 RGGWARTFGRRFERSAGGEAAPSFDGHLAGAQLGADLYARSSATRHTDAFGVFGGYATVR 2162

Query: 466 STFHN---PDTDNLLTGNVKFGAGVYATWHQLQDKQTGAYADSWMQMQRFRHINTEDG 522
 H + + T ++ G Y T G Y D+ + R+R + +
 Sbjct: 2163 GDVHGLARGEIQAVGTSTLRATQLGAYWT---HTGPGGWYIDTVLAGTRYRQQTKSSAQ 2218

Query: 523 TERFTSK-GITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDSENAHV 581
 + G+TAS+EAGY L + R ++PQAQ+ Y + + V
 Sbjct: 2219 VGAWSRGWGMTASVEAGYPWQL-----NPRWRIEPQAQVYQQLGIANGADRVSTV 2269

Query: 582 NLLGSRQLQTRGVVQAKAQFSLYKNIAIEPFAAVNALY-----HNKPGVEMDGER 632
 + L R+G + Q++ Y + PF V+ L+ GV +
 Sbjct: 2270 SYKTPDALTARLGTRLSGQYA-YGKAQLRPFMGVSLLHDFTGADTVTFAGAHGVRASRQN 2328

Query: 633 RVINNKTAIESQLGVAV 649
 ++ K +++QLG +V
 Sbjct: 2329 TAVDLKAGVDTQLGKSV 2345

tr Q7WHU5 Autotransporter [BB3111] [Bordetella bronchiseptica] 528
 (Alcaligenes AA
 bronchisepticus) align

Score = 53.5 bits (127), Expect = 1e-05
 Identities = 55/220 (25%), Positives = 89/220 (40%), Gaps = 42/220 (19%)

Query: 478 TGNVKGFGAGVYATWHQLQDKQTGAYADSMQYQFRHRINTEDGTER-----FTSKGIT 532
TG G YAT+ + G Y D ++ R+ H D R + + G+
Sbjct: 328 TGEGDSVHVGAYATYIE----DGGFYMDGIVRVARYAHEFKAPDAKGRVRGKYRANGVG 383

Query: 533 ASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLT-YLGVNGKFSDESEAHVNLLGSRQLQT 591
AS+E G + FT G Y++PQ ++ + G + ++ V G L
Sbjct: 384 ASLELG-----KRFTWAG---AWYVEPQLEMAVFHAQGGSYRAGQDLRVKDNLTSLLG 434

Query: 592 RVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRV---INNKTAI----E 642
RVG+ QF L ++P+A ++ L E DG+ V + +K+ + E
Sbjct: 435 RVGLHVGRQFDLGDGRVVQPYAKLSWLQ-----EFDGKNTVRTNGVRHKSRLDGGRAE 487

Query: 643 SQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682
LGVA ++ H +L G + AK + WTF
Sbjct: 488 LDLGVAAGLGKHGSLY-----GSYEYAKGSRQTMPWTF 520

tr Q7WC76 Autotransporter [BPP0452] [Bordetella parapertussis] 1769 AA align

Score = 53.5 bits (127), Expect = 1e-05
Identities = 58/257 (22%), Positives = 103/257 (39%), Gaps = 29/257 (11%)

Query: 408 KGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQR 465
+G W R + G+ AP +G+ G QLG +++ + + + G+ GG A R
Sbjct: 1495 RGGWARTFGRRFERSAGGEAAPSFDGHLAGAQLGADLYARSSGTRHTDAFGVFGGYATVR 1554

Query: 466 STFH-----PDTDNLTGKVGFAGVYATWHQLQDKQTGAYADSMQYQFRHRINTEDG 522
H + + T ++ G Y T G Y D+ + R+R + +
Sbjct: 1555 GDVHGLARGEIQAVGTSTLRATQLGAYWT----HTGPGGWYIDTVLAGTRYRQQTKSSAQ 1610

Query: 523 TERFTSK-GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDESEAHV 581
+ G+TAS+EAGY L + R ++PQAQ+ Y + + V
Sbjct: 1611 VGAVSRGWMGTASVEAGYPWQL-----NPRWRIEPQAQVYYQQLGIANGADRVSTV 1661

Query: 582 NLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY-----HNKPGVEMDGER 632
+ L R+G + Q++ Y + PF V+ L+ GV +
Sbjct: 1662 SYKTPDALTARLGTRLSGQYA-YGKAQLRPFMGVSLLHDFTGADTVTFAGAHGVRASRQN 1720

Query: 633 RVINNKTAIESQLGVAV 649
++ K +++QLG +V
Sbjct: 1721 TAVDLKAGVDTQLGKSV 1737

tr Q8VV95 Vag8 protein (Autotransporter) [vag8-2] [Bordetella pertussis] 915 AA

align

Score = 52.0 bits (123), Expect = 4e-05
Identities = 61/252 (24%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGKVGFAGVYATWHQL 495
G++LG + + S+G++ G +E R D G+V G Y ++ L
Sbjct: 678 GIELGLDRRVAGGATTAWSVGMLAGYSETRR----DGGAYRAGHVHSAGVGAYVSY--L 730

Query: 496 QDKQTGAYADSWMQYQRFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
 D +G+Y D ++Y RFRH I T D + S G+ A + G + +
 Sbjct: 731 ND--SGSYVGVVKYNRFRHGFDIRTDLKRVDAKRSRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAI 609
 Y++PQA + + G ++ S V G+ R G +A Q L +
 Sbjct: 786 -----YVEPQASVAWFHAGGSRYEASNGLRVRADGAHSWVLRAGAEAGRQMRMLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
 EP+A A NA+Y N G R V ++ E++GV + L A
 Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
 + G +A
 Sbjct: 892 DYELYAKGARFEA 903

tr 066044 Vag8 [vag-8] [Bordetella pertussis] 915 AA
align

Score = 52.0 bits (123), Expect = 4e-05
 Identities = 61/252 (24%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTNLTTGNVKFGAGVYATWHQL 495
 G++LG + + S+G++ G +E R D G+V G Y ++ L
 Sbjct: 678 GIELGLDERRVAGGATTAWSGMLAGYSETRR-----DGGAYRAGHVHSAGVAYVSY--L 730

Query: 496 QDKQTGAYADSWMQYQRFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
 D +G+Y D ++Y RFRH I T D + S G+ A + G + +
 Sbjct: 731 ND--SGSYVGVVKYNRFRHGFDIRTDLKRVDAKRSRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAI 609
 Y++PQA + + G ++ S V G+ R G +A Q L +
 Sbjct: 786 -----YVEPQASVAWFHAGGSRYEASNGLRVRADGAHSWVLRAGAEAGRQMRMLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
 EP+A A NA+Y N G R V ++ E++GV + L A
 Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
 + G +A
 Sbjct: 892 DYELYAKGARFEA 903

tr Q7WQ83 Autotransporter [BB0450] [Bordetella bronchiseptica 2152
 (Alcaligenes AA
 bronchisepticus)] align

Score = 51.6 bits (122), Expect = 5e-05
 Identities = 47/220 (21%), Positives = 88/220 (39%), Gaps = 23/220 (10%)

Query: 407 RKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQLSI-GLMGGQAEQ 464
 R+G W R + G P +G+ G+Q G + + + + + G+ GG A
 Sbjct: 1876 RRGAWTRAFGRTFERSGSGDVEDPRFDGHVAGLQAGVDLYARRSDQGHADLAGVFGGYANA 1935

Query: 465 RSTFHNPDTDNLTGNGVKFGA-----GVYATWHQLQDKQTGAYADSWMQYQRFRHRI-N 518
 R D G + Y + +G Y D+ + R+ + +
 Sbjct: 1936 RGHM-----DGFARGETGAYAGKPDLNAYYIGGYWTHIGPSGWYVDAVLAGTRYEQKAKS 1990

Query: 519 TEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDE 578
 + D G+TAS+EAGY + E + +++PQAQL Y + + +
 Sbjct: 1991 SNDLRTEAKGWGVTASVEAGYPVPIGEKW-----HIEPQAQLVYQRLTVSNGEDDV 2041

Query: 579 AHVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNAL 618
 + V+ + R+G + Q++ Y + PF V+ L
 Sbjct: 2042 SSVSYRTPDSVTARLGARLSGQYA-YNTTQLRPFMEVSL 2080

tr Q7WC79 Autotransporter [BPP0449] [Bordetella parapertussis] 1616 AA align

Score = 51.6 bits (122), Expect = 5e-05
 Identities = 47/220 (21%), Positives = 88/220 (39%), Gaps = 23/220 (10%)

Query: 407 RKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQLSI-GLMGGQAEQ 464
 R+G W R + G P +G+ G+Q G + + + + + + + G+ GG A
 Sbjct: 1340 RRGAWTRAFGRTFERSGSGDVPDPRFDGHVAGLQAGVLDYARRSDQGHADLAGVFGGYANA 1399

Query: 465 RSTFHNPDTDNLTGNGVKFGA-----GVYATWHQLQDKQTGAYADSWMQYQRFRHRI-N 518
 R D G + Y + +G Y D+ + R+ + +
 Sbjct: 1400 RGHM-----DGFARGETGAYAGKPDLNAYYIGGYWTHIGPSGWYVDAVLAGTRYEQKAKS 1454

Query: 519 TEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDE 578
 + D G+TAS+EAGY + E + +++PQAQL Y + + +
 Sbjct: 1455 SNDLRTEAKGWGVTASVEAGYPVPIGEKW-----HIEPQAQLVYQRLTVSNGEDDV 1505

Query: 579 AHVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNAL 618
 + V+ + R+G + Q++ Y + PF V+ L
 Sbjct: 1506 SSVSYRTPDSVTARLGARLSGQYA-YNTTQLRPFMEVSL 1544

tr Q7W9Y1 Autotransporter [BPP1618] [Bordetella parapertussis] 519 AA align

Score = 51.6 bits (122), Expect = 5e-05
 Identities = 57/243 (23%), Positives = 92/243 (37%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTGNGVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 301 VGAVAGYTNGRIKF----DRGGTGDDDSVHVGAYATYIE---DGGFYMDGIVRVSIR 351

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 352 HAFKVDDAKGRRVRGQYRGNGVGASLELG----KRFTWPG---AWYVEPQLEVAAFRA 402

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 403 QGADYTASNGLRIKDDGNTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 455

Query: 629 DGERRVINNKT-----AIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V N E LGVA ++ H +L G + AK +
 Sbjct: 456 DGKGTVRTNGVRHKNRLDGGRALDLGVAAQLGKHGSLY-----GSYEYAKGSRQTMP 508

Query: 680 WTF 682
 WTF
 Sbjct: 509 WTF 511

tr Q9F290 **YapC protein (Putative autotransporter) (Putative autotransporter protein) [yapC] [Yersinia pestis]** 638
 AA
align

Score = 51.2 bits (121), Expect = 6e-05
 Identities = 39/205 (19%), Positives = 90/205 (43%), Gaps = 22/205 (10%)

Query: 409 GLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTF 468
 G+W R + S + K + G+++G + N N L + +
 Sbjct: 382 GVWARYLTDDS-RLSDNKNIAFKNTLSGMEIGADKQLGLNRGNMLIGAFTSYSSSDVKST 440

Query: 469 HNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDGTERFTS 528
 H+ + G+++ +G G+Y T+ Q+G Y D+ ++ RF +++NT++ +
 Sbjct: 441 HDAN-----GDIRSYGGGLYLTYLD---QSGFYVDTVLKANRFNNKMNTQETRGEYNQ 490

Query: 529 KGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV-NGKFSDENAHVNLGSR 587
 +T S+E+GY + + + L+P +++Y + + ++ S + +
 Sbjct: 491 NALTTSVESGYQWPVYAN-----LVLEPYGKVSYSRIGSADYTLSNGMVAEVAKAD 541

Query: 588 QLQTRGVQAKAQFSLYKNIAIEPF 612
 +Q +G A +S+ + I+P+
 Sbjct: 542 SVQGELGTVLAASYSI-NQMTIKPY 565

tr Q881D0 **Outer membrane autotransporter [PP3069] [Pseudomonas putida (strain KT2440)]** 825
 AA
align

Score = 50.8 bits (120), Expect = 8e-05
 Identities = 57/222 (25%), Positives = 97/222 (43%), Gaps = 36/222 (16%)

Query: 477 TTGNVKGFAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDG-TERFTSKGITASI 535
 + G++K G V W + + GAY D+ +QY R R +E G T TAS+
 Sbjct: 624 SVGDLKLDGDSVGTWTLVGPQ--GAYLDAVLQYTRLDGRARSERGDTLNLDGHAWTASL 681

Query: 536 EAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDENAHVNLGSRQLQTRGV 595
 E+GY L+E R ++PQAQL V + + + ++ +L R+G+
 Sbjct: 682 ESGYPITLSE-----RWRVEPQAQLIAQKVALESARDSVSRISHDAQVELTGRLGL 732

Query: 596 QAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVIN-----NKTAIESQ 644
 + + F+ ++PFA VN L+H DG R + T+++ +
 Sbjct: 733 RLEGAFTGSSGRLLQPFAQVN-LWHG-----DGGRDTLTFDDADKIKTDYRTSVQLE 784

Query: 645 LGVAVKIKSHLTL---QATFNRQTGKHHQAKQGALNLQWTF 682
 GV ++ L+L Q T N + + +A L ++W F
 Sbjct: 785 SGVVAQVNEALSLHGGVQYTANLDS-RQQEASGVNLGVRWQF 825

sp P76017 Hypothetical protein *ycgV* [*ycgV*] [*Escherichia coli*] 955 AA align

Score = 50.1 bits (118), Expect = 1e-04

Identities = 58/218 (26%), Positives = 94/218 (42%), Gaps = 32/218 (14%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
+WLR G + + GK + + G+Q GG+ ++ L +GL G ST

Sbjct: 694 IWLRSYGGSLDSFASGKLSGFDMGYSGIQFGGD--KRLSDVMPLYVGLYIG----STHA 746

Query: 470 NPDTDNLTGKGFAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDG----TE 524
+PD G + G+YA++ Q G Y+D ++ R ++ + D

Sbjct: 747 SPDYSG-GDGTARSODYMGMYASYM---AQNGFYSDLVIAKASRQKNSFHVLDSQNNGVNA 801

Query: 525 RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHV 581
T+ G++ S+EAG + F Y++PQ QLTY N K S+ N H+

Sbjct: 802 NGTANGMSISLEAG----QRFNLSPTGYGFYIEPQTQLTYSHQNEMTMKAASNGLNIHL 855

Query: 582 N---LLGSRQLQTRGVQKAQFSLY-KNIAIEPFA 613
N LLG + + A +Q ++Y K AI F+

Sbjct: 856 NHYESLLGRASMILGYDITAGNSQLNVYVKTGAIREFS 893

tr Q881W9 Autotransporter, putative [PSPT02763] [*Pseudomonas syringae*] 927
(pv.
tomato)] AA align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 69/290 (23%), Positives = 112/290 (37%), Gaps = 39/290 (13%)

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQ-LSIGLMGGQAEQ--- 464
W RV Q G +P ++ KG Q+G +V+ W + Q L IGL Q

Sbjct: 657 WARVFGSDKQQWSGTVSPGLDASLKGYQIGHDVYAWSLDGQQILRIGLFVAQNRLDGKV 716

Query: 465 ---RSTFHNPDTDNLTGKGFAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED 521
FH TG +K G V A W T +Y D+ + R ++

Sbjct: 717 QGFAGGFHARH----TGRIKLHGDSVGAYW--TLSSPTASYVDALVMSTRLDGYSRSDR 769

Query: 522 GTERFTSKG--ITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579
G R ++G ++ S+EAG+ +L R +PQ Q+ + ++ +

Sbjct: 770 GL-RIDTQGHALSLSVEAGHPFVLTP-----RWVAEPQVQIHIQRIDLDDQHDGIS 819

Query: 580 HVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNK--PFGVEMDGERRVINN 637
HV R+G++ K +++L + IEP+ N L+ N V D R+

Sbjct: 820 HVGFDSPQYNTGRLGIRFKGRYAL-AGMPIEPYLRAN-LWRNAGGHDVTFDHTERIKTA 877

Query: 638 KTAIESQLGVAVKIK---SHLTLQATFNRQTGKHHQAKQGA---LNLQW 680
+ LG + IK + + A +NR H + A + L W

Sbjct: 878 HRSTTGSLGAGMVIKVASDTSVYWGADYNRDLNSHDSSGANASLGVR LAW 927

tr Q7WL85 Autotransporter [vag8] [Bordetella bronchiseptica (Alcaligenes bronchisepticus)]

align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 59/252 (23%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQL 495
 G++LG + + S+G++ G +E R D G+V G Y ++ L
 Sbjct: 678 GIELGIDRRVAGGATTAWSVGMLAGYSETRR----DGGAYRAGHVHSAGVSY--L 730

Query: 496 QDKQTGAYADSWMQMQRFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
 D +G+Y D ++Y RFRH + T D + S G+ A + G + +
 Sbjct: 731 ND---SGSYVDGVVVKYNRFRHGFDVRTDLKRVDAKRSRSHGLGALLRGGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAI 609
 Y++PQA + + +G ++ S V + R G +A Q L +
 Sbjct: 786 -----YVEPQASVAWFHADGSRYEASNGLRVRADSAHSWVLRAGAEAGRQMRLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
 EP+A A NA+Y N G R V ++ E+++GV + L A
 Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
 + G +A
 Sbjct: 892 DYELYAKGARFEA 903

tr Q7W7U5 Autotransporter [vag8] [Bordetella parapertussis] 915 AA

align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 59/252 (23%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQL 495
 G++LG + + S+G++ G +E R D G+V G Y ++ L
 Sbjct: 678 GIELGIDRRVAGGATTAWSVGMLAGYSETRR----DGGAYRAGHVHSAGVSY--L 730

Query: 496 QDKQTGAYADSWMQMQRFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
 D +G+Y D ++Y RFRH + T D + S G+ A + G + +
 Sbjct: 731 ND---SGSYVDGVVVKYNRFRHGFDVRTDLKRVDAKRSRSHGLGALLRGGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAI 609
 Y++PQA + + +G ++ S V + R G +A Q L +
 Sbjct: 786 -----YVEPQASVAWFHADGSRYEASNGLRVRADSAHSWVLRAGAEAGRQMRLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
 EP+A A NA+Y N G R V ++ E+++GV + L A
 Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
 + G +A
 Sbjct: 892 DYELYAKGARFEA 903

tr Q7WHU6 Autotransporter [BB3110] [Bordetella bronchiseptica] 770
 (Alcaligenes AA
 bronchisepticus)] align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 552 VGAVAGYTNNGRIKF----DRGGTGDDDSVHVGAYATYIE---DGGFYMDGIVRVSIR 602

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 603 HAFKVDDAKGRRVRGQYRGNGVGASLELG----KRFTWPG---AWYVEPQLEVAAFHA 653

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 654 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ----EF 706

Query: 629 DGERRV----INNKTAI----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 707 DGKGTVRTNDIRHKVRLDGGRALAVGVASQLGKHGSL----FGSYEYAKGSRQTMP 759

Query: 680 WTF 682
 WTF
 Sbjct: 760 WTF 762

tr O86135 Tracheal colonization factor precursor [tcfA2] [Bordetella 647 AA pertussis] align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 429 VGAVAGYTNNGRIKF----DRGGTGDDDSVHVGAYATYIE---DGGFYMDGIVRVSIR 479

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG----KRFTWPG---AWYVEPQLEVAAFHA 530

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ----EF 583

Query: 629 DGERRV----INNKTAI----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 584 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682
 WTF
 Sbjct: 637 WTF 639

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 429 VGAVAGYTNGRIKF----DRGGTGDDDSVHVGAYATYIE---DGGFYMDGIVRVSIR 479

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG----KRFTWPG---AWYVEPQLEVAAFHA 530

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ----EF 583

Query: 629 DGERRV----INNKTAI----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 584 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682
 WTF
 Sbjct: 637 WTF 639

tr Q9F4B3 BapB protein [bapB] [Bordetella pertussis] 482 AA align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 264 VGAVAGYTNGRIKF----DRGGTGDDDSVHVGAYATYIE---DGGFYMDGIVRVSIR 314

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 315 HAFKVDDAKGRRVRGQYRGNGVGASLELG----KRFTWPG---AWYVEPQLEVAAFHA 365

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 366 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ----EF 418

Query: 629 DGERRV----INNKTAI----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 419 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL----FGSYEYAKGSRQTMP 471

Query: 680 WTF 682
 WTF
 Sbjct: 472 WTF 474

tr Q8GB90 Tracheal colonization factor [tcfA] [Bordetella pertussis] 647 AA

align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 429 VGAVAGYTNNGRIKF-----DRGGTGDDDSVHVGAYATYIE----DGGFYMDGIVRVSIR 479

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 530

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 583

Query: 629 DGERRV---INNKTAI-----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 584 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682
 WTF
 Sbjct: 637 WTF 639

tr Q45343 Tracheal colonization factor [tcfA] [Bordetella pertussis] 672 AA

align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 454 VGAVAGYTNNGRIKF-----DRGGTGDDDSVHVGAYATYIE----DGGFYMDGIVRVSIR 504

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 505 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 555

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 556 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 608

Query: 629 DGERRV---INNKTAI-----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 609 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 661

Query: 680 WTF 682
 WTF
 Sbjct: 662 WTF 664

tr Q6U948 Tracheal colonization factor protein [tcfA] [Bordetella pertussis] 642
 AA
align

Score = 49.3 bits (116), Expect = 2e-04
 Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 424 VGAVAGYTNNGRIKF-----DRGGTGDGSVHVGAYATYIE----DGGFYMDGIVRVSIR 474

Query: 515 HRINTEDGTER----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 475 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 525

Query: 570 NG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 526 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 578

Query: 629 DGERRV----INNKTAI----ESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQ 679
 DG+ V I +K + E +GVA ++ H +L G + AK +
 Sbjct: 579 DGKGTVRTNDIRHKVRLDGGRTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 631

Query: 680 WTF 682
 WTF
 Sbjct: 632 WTF 634

tr Q7WKS2 Putative autotransporter [bapC] [Bordetella bronchiseptica] 993 AA
 (Alcaligenes bronchisepticus) align

Score = 48.1 bits (113), Expect = 5e-04
 Identities = 96/486 (19%), Positives = 174/486 (35%), Gaps = 80/486 (16%)

Query: 234 GQTISLDEFRLENSWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
 G T +++ R+E+ W S V L + + T +ES L VK +G
 Sbjct: 543 GITNTVNALRIEDGTWTGSSAVNSLHLQAGKVAYATPAESDGKFKHLRVKT-LSGSGL 601 ,

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSIDIFENP-----IDDLKSLD-----GHQIIKV 334
 F + L+ +G ++ ++ L ++ G +
 Sbjct: 602 FEMNASADLSDGDLLVVSDEASGQHKVLVRGAGTEPTGVESLTVELPKGSQAGFTLANR 661

Query: 335 NGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKN-----AMIWRFMHNRKPPIP 387
 G D AFR G++ L + + N + IW N L +
 Sbjct: 662 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIWYAEGLNSKRLG 721

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHHSNQWVQGKTAPVEGYRKGVQ--LGGEVFT 445
 LRL+ + RT +K + +D + + K V G+ G + G+
 Sbjct: 722 -ELRLDPGAGGFWGRTFAQK---QQLDNKAGRRFDQK---VYGFELGADHAIAGQQGR 772

Query: 446 WQNESNQLSIGLGGQAEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYAD 505
 W +G + G R +F + + + ++ + A V G Y D
 Sbjct: 773 WH-----VGGLLGYTRARRSFVDDGAGHTDSAHIIGAYAAYV-----ADNGFYFD 816

Query: 506 SWMQYQRFRH--RINTEDGTE---RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQP 560
 S ++ RF + + D ++ + G+ A++EAG L + + + +P

Subjct: 817 STLRASRFENDFTVTATDAVSIRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 867

Query: 561 QAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVGVQAKAQFSLYKNIAIEPFAAVNALY 619
Q++++ +G + + N V G R+G+ A + L K+ I+P+A ++ L

Subjct: 868 QSEVSLFHASGGTYRAANNLSVKDEGGTSAVRLGLAAGRRIELGKDRVIQPYATLSWLQ 927

Query: 620 HNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTQATFNRQ---TGKHHQAKQGAL 676
E G V N + + LG + + L L A R + AK L

Subjct: 928 -----EFKGVTTVRTNGYGLRTDLG-GGRAELALGLAAALGRGHKFYT SYEYAKGNKL 979

Query: 677 NLQWTF 682

L WTF

Subjct: 980 TLPWTF 985

tr Q83RP3 Putative adhesion and penetration protein [SF1205] [Shigella flexneri] 955 AA

align

Score = 47.4 bits (111), Expect = 0.001

Identities = 57/218 (26%), Positives = 93/218 (42%), Gaps = 32/218 (14%)

Query: 410 LWLRVIDGHNSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
+WLR G + + GK + + G+Q GG+ ++ L +GL ST

Subjct: 694 IWLRSYGGSLDSFASGKLSGFDMGYSGIQFGGD--KRLSDVMPLYVGLY----IDSTHA 746

Query: 470 NPDTDNLTGKVKGFGAGVYATWHQLQDKQTGAYADSWM QYQRFRHRINTEDG----TE 524
+PD G + G+YA++ Q G Y+D ++ R ++ + D

Subjct: 747 SPDYSG-GDGTARSODYMGMYASYM---AQNGFYSDLVIKASRQKNSFHVLDSQNNGVNA 801

Query: 525 RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAKQFSLYLGVNG---KFSDSENAHV 581
T+ G++ S+EAG + F Y++PQ QLTY N K S+ N H+

Subjct: 802 NGTANGMSISLEAG----QRFNLSPTGYGFYIEPQTQLTYSHQNE MAMKASNGLNIHL 855

Query: 582 N----LLGSRQLQTRGVQKAQFSLY-KNIAIEPFA 613

N LLG + + A +Q ++Y K AI F+

Subjct: 856 NHYESLLGRASMILGYDITAGNSQLNVYVKTGAIREFS 893

tr Q7WK68 Autotransporter [BB2270] [Bordetella bronchiseptica] . 559
(Alcaligenes
bronchisepticus)] AA

align

Score = 47.4 bits (111), Expect = 0.001

Identities = 50/219 (22%), Positives = 85/219 (37%), Gaps = 42/219 (19%)

Query: 479 GNVKGFGAGVYATWHQLQDKQTGAYADSWM QYQRFRHRINTEDG----TERFTSKITA 533
GN G YAT+ G Y D ++ R+ H + T ++ + GI

Subjct: 360 GNSDSLHV GAYATYIG---DGGFYLDGIVRVNRYEHDFKADGQRGARVTGKYRANGIGL 415

Query: 534 SIEAGYNALLAEHFTKKGNSLRVYLQPQAKQFSLYLGVNGK-FSDSENAHVNLGSRQLQTR 592
S+E G FT G+ +++PQ ++ G ++ S V++ ++ L R

Subjct: 416 SLETG-----RRFTWAGDW---FVEPQVEVALFRSGGADYTASNGVRVDVASTKSLLGR 466

Query: 593 VGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTA-----IES 643

G+Q + L ++P+A ++ L E DG +V N E
Sbjct: 467 AGLQVGRKLDLGNGLVQPYAKLSWLQ-----EFDGVGKVRTNDIGHDVKLRGGRAEL 519

Query: 644 QLGVAVKIKSHLTLQATFNRQQTGKHHQAKQGALNLQWTF 682
 LGVA + H +L A++ G L + W+F
Sbjct: 520 DLGVAAALGRHSSLFASAYEYSKGSR-----LTIPWSF 551

tr Q7VVD6 Autotransporter (Pseudogene) [bapC] [Bordetella pertussis] 993 AA

align

Score = 47.4 bits (111), Expect = 0.001

Identities = 93/486 (19%), Positives = 173/486 (35%), Gaps = 80/486 (16%)

Query: 234 GQTISLDEFRLLENSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
G T +++ R+E+ W S V L + + T +ES L VK +G
Sbjct: 543 GMTKTVNALRIEDGTWTGGSSTVNSLHLQAGKVAYATPAESDGEFKHLRVK-TLSGSGI 601

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSDDIFENPIDDLKSLDGHQIIKV----- 334
 F + L+ +G ++ + ++ +++++
 Sbjct: 602 FEMMNASADLSDGDLIIVYCGEASCGQKVLVPGACTERTGCVESLTIVELRECGGOTKETLND 661

Query: 335 NGTADKHAFLSGKHQKGIYTLSLQQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
 G D AFR G++ L + N + IW N L +
 Subject: 560 GQHIVLQAFRNLQFLGKQKGIYTLSLQQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQ -- LGGEVFT 445
LRL+ + RT +K + +D + + K V G+ G + G+

Query: 446 WQNESNQLS IGLMGGQAEQRSTFHNPDTDNLTGNVKGFAGVYATWHQLQDKQTGAYAD 505
W +G + G R +F + + + + + A V G Y D

Query: 506 SWMQYQRFRH--RINTEDGTE---RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLOP 560

S ++ RF + + D ++ + G+ A++EAG L + + +++P
Sbjct: 817 STLRASRFENDFTVTATDAVSRGKYRANGVGAITLEAGKRTLHDGW-----FVEP 867

Query: 561 QAQLT-YLGVNGKFSDSENAHVNLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY 619
 Q+++++ + G + + N V G R+G+ A + L K+ I+P+A ++ L
 Sbjct: 868 QSEVSLFHASGGTYRAANNLSQLVKDEGGTSAVLRLGLAAGRRLIDLGKDRVIAQYATL-SWLQ 927

Query: 620 HNKPGVEMDGERVINNKTAIESQLGVAVKIKSHLTLQATFNR -- QTGKHHQAKQGAL 676
 E G V N + + L + + L L A R + AK L
 Sbjct: 828 DEKSYLTTEVNTGCLRTTLCGCGAAEVLNGLANLGCQHQLVTCVHVNKCNKQ

Quay: 677 NLOWTE 683

NLQWTF

L WTF

tr Q7C1Y6 Putative adhesion and penetration protein [S1289] [Shigella flexneri]

align

S+E G FT G+ +++PQ ++ L +GK ++ S V++ ++ L
 Sbjct: 395 SLETG-----RRFTWAGDW---FVEPQVEVA-LFRSGKADYTASNGVRVDVASTKSLLG 444

Query: 592 RVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINKTA-----IE 642
 R+G+Q + L ++P+A ++ L E DG +V N E
 Sbjct: 445 RLGLQVGRKLDLGNGKLVQPYAKLSWLQ-----EFDGVGKVRTNDIGHDVKLRGGRAE 497

Query: 643 SQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682
 LGVA + H +L A++ G L + W+F
 Sbjct: 498 LDLGVAAALGKHSSLFASYEYSKGSR-----LTIPWSF 530

tr Q7W1F5 Autotransporter [BPP0735] [Bordetella parapertussis] 984 AA
align

Score = 46.2 bits (108), Expect = 0.002
 Identities = 72/280 (25%), Positives = 110/280 (38%), Gaps = 39/280 (13%)

Query: 407 RKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNE---SNQLSIGLMGGQA 462
 RK W RVI Q G P +G Q G ++ + S++L + GQA
 Sbjct: 711 RKAGWGRVIGQRLTQRWDGDVEPRFKGNIWIAQAGADMLERDRDDGLSDRLGLFSAYGQA 770

Query: 463 EQRSTFHNPDTDNLTTGN--VKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTE 520
 + R G V+ +G G+Y W +L K T Y D+ + + R ++
 Sbjct: 771 DGRVDGFWQGEHGKQAGKLRVEAYGLGLY--WTRL--KHTNWYWDNVLMGNYYTGRSRSD 826

Query: 521 DGTER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579
 G G TAS EAGY+ H + LQPQAQL Y +++ +N
 Sbjct: 827 RGVAASLEGWGFTASSEAGYS-FFPRH-----DIMLQPQAQLVY----QYTSLDNT 872

Query: 580 H-----VNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRV 634
 H + G L R+G+ + + I P+A +N L+H GE
 Sbjct: 873 HDAYSTIRYHGGALTGRIGLLLQGNADQPER--IRPYARIN-LWHR----FSHGESVS 924

Query: 635 INNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQG 674
 +I ++ G + + + L A NRQT + A G
 Sbjct: 925 FGPSDSIRTEYG-STSMMDLRIGLAAPLNQTELYASAGYG 963

tr Q7WP64 Autotransporter [BB0821] [Bordetella bronchiseptica]
 (Alcaligenes
 bronchisepticus)] 987
AA
align

Score = 45.4 bits (106), Expect = 0.003
 Identities = 71/275 (25%), Positives = 106/275 (37%), Gaps = 29/275 (10%)

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLS--IGLMG--GQA 462
 RK W RVI Q G P + G ++ + LS +GL G GQA
 Sbjct: 714 RKAGWGRVIGQRLTQRWDGDVEPRFKGNIWIAQAGADMLERDRDDGLSDRLGLFGAYGQA 773

Query: 463 EQRSTFHNPDTDNLTTGN--VKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTE 520
 + R G V+ +G G+Y W +L K T Y D+ + + R ++
 Sbjct: 774 DGRVDGFWQGEHGKQAGKLRVEAYGLGLY--WTRL--KHTNWYWDNVLMGNYYTGRSRSD 829

Query: 521 DGTER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579

G G TAS EAGY+ H + LQPQAQL Y + + +
 Sbjct: 830 RGVAASLEGWGFTASSEAGYS-FFPRH-----DIMLQPQAQLVYQYTSLEDDTHDAYS 880

Query: 580 HVNLLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNKT 639
 + G L R+G+ + + I P+A +N L+H GE
 Sbjct: 881 TIRYHGGALTGRIGLLLQGNADQPER--IRPYARIN-LWHR-----FSHGESVSFGPSD 932

Query: 640 AIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQG 674
 +I ++ G + + + L A NRQT + A G
 Sbjct: 933 SIRTEYG-STSMDLRIGLAAPLNRQTELYASAGYG 966

tr Q6G430 Hypothetical protein [BH05490] [Bartonella henselae] 1291
 (Rochalimaea
 henselae)] AA
align

Score = 44.3 bits (103), Expect = 0.008
 Identities = 55/225 (24%), Positives = 91/225 (40%), Gaps = 42/225 (18%)

Query: 479 GNVKG---FGAGVYATWHQLQDKQTGAYADSMQYQRFRHRINTEDGTE----RFTSKG 530
 G V G + G YAT+ ++G Y DS ++Y +++++ + + G
 Sbjct: 1088 GGVSGINTYSIGAYATYFD---KSGWYLDLSILKYNQYQNNLKAVSTNGIAIEGNYNQWG 1143

Query: 531 ITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHVNLGSR 587
 + S EAGY TK ++QP AQL+L V G K S+ +N S
 Sbjct: 1144 LGTSFEAGYRF---ETTKSS----WMQPYAQLSWLQVEGKEIKLSNEMTGDINAFTS- 1193

Query: 588 QLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNKTAIESTL-- 645
 L++ VG+ A +F L ++ + L N+ D R IN + L
 Sbjct: 1194 -LRSEVGLSAGYEFCLGGDVTSMAYITAAWLRENR-----DSNRTTINKLHQFVTDLSG 1246

Query: 646 -----GVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 G++ + L A G K Q+ QG L +++++F
 Sbjct: 1247 NFGKLGIGLSSLVSKKFKLYAEAQYVKGDVKQSFQGILGVRYSF 1291

tr Q7W7D4 Putative autotransporter [bapC] [Bordetella parapertussis] 986 AA
align

Score = 44.3 bits (103), Expect = 0.008
 Identities = 93/485 (19%), Positives = 172/485 (35%), Gaps = 80/485 (16%)

Query: 234 GQTISLDEFRLENSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
 G T +++ R+E+ W S V L + + T +E+ L VK +G
 Sbjct: 536 GITKTVNALRIEDGTWTGSSAVNSLHLQAGKVAYATPAETNGKFKHLRVKT-LSGSGL 594

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSIIIFENP-----IDDLKSLD-----GHQIIKV 334
 F + L+ +G ++ ++ L ++ G +
 Sbjct: 595 FEMNASADLSDGDLVVSDEASGQHKVLVRGAGTEPTGVESLTLVELPKGSQAGFTLANR 654

Query: 335 NGTADKHAFLSGKHQKGIYTLSLQQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
 G D AFR G++ L + N + IW N L +
 Sbjct: 655 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIWIYAKGNALSKRLG 714

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQ--LGGEVFT 445
 LRL+ + RT +K + +D + + K V G+ G + G+
 Sbjct: 715 --ELRLDPGAGGFWGRTFAQK---QQLDNKAGRRFDQK---VYGFELGADHAIAGQQGR 765

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVYATWHQLQDKQTGAYAD 505
 W +G + G R +F + + + ++ + A V G Y D
 Sbjct: 766 WH-----VGGLLGYTRARRSFVDDGAGHTDSAHIAGAYAAYV-----ADNGFYFD 809

Query: 506 SWMQYQRFRH--RINTEDGTE--RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQP 560
 S ++ RF + + D ++ + G+ A++EAG L + + +++P
 Sbjct: 810 STLRASRFENDFTVTATDAVSIRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 860

Query: 561 QAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALY 619
 Q+++ +G + + N V G R+G+ + L K+ I+P+A ++ L
 Sbjct: 861 QSEVSLFHASGGTYRAANNLSVKDEGGTSAVLRLGLATGRRIDLGKDRVIQPYATLSWLQ 920

Query: 620 HNKPGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTG---KHHQAKQGAL 676
 E G V N + + LG + + L L A R + AK L
 Sbjct: 921 -----EFKGVTTVRTNGYGLRTLG-GGRAELALGLAAALGRGHSLYTSYEAKGSKL 972

Query: 677 NLQWT 681
 L WT
 Sbjct: 973 TLPWT 977

tr Q9JMS5 **ycbB protein [ycbB] [Escherichia coli]** 1758 AA
align

Score = 43.5 bits (101), Expect = 0.013
 Identities = 29/112 (25%), Positives = 54/112 (47%), Gaps = 12/112 (10%)

Query: 437 VQLGGEVFTWQNESNQLSIGLMG--GQAEQRSTFHNPDTDNLTTGNVKFGAGVYATWHQ 494
 + +GG+++ W + N IG+MG G A ++T N + TGIV G+ G+Y + Q
 Sbjct: 1499 MMIGGDIYNWTDGYNYSHIGIMGGMGSAAKTTSTN---NKRATGNVDGYTLGLYHVFQQ 1555

Query: 495 -----LQDKQTGAYADSWMQYQRFRHRI-NTEDGTERFTSKGITASIEAGY 539
 + ++ G + S +QY + + + +T + + G + E GY
 Sbjct: 1556 NISDGLNESERQGLWTYSSIQYMDYDNSVSSTNNFKANYGVNGFRLTGEVGY 1607

tr Q9XD84 **TibA [tibA] [Escherichia coli]** 989 AA
align

Score = 43.1 bits (100), Expect = 0.017
 Identities = 50/210 (23%), Positives = 86/210 (40%), Gaps = 26/210 (12%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGEVFTWQNESNQ 452
 L ++ D+ T G+W R G N+ G ++ + G + G ++ ++S+
 Sbjct: 711 LRFRHGDVMQNTRAPGGVWGRYT-GSDNRISGGASSGYLTQNGFETGADMVFDSLSDSS- 768

Query: 453 LSIGLMGGQAEQRSTFHNPDTDNLTTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQR 512
 L++G ++ S H + NV G G+YATW G Y D ++Y R
 Sbjct: 769 LAVGTFFSYSDN-SIKHARGGKS---NVDSSGGGLYATWFD---NDGYYVDGVLKYNR 819

Query: 513 FRHRINT--EDGTE--RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYL 567

F + + T DGT ++ G S+EAG L E+ + QP + T
 Sbjct: 820 FNNEELRTWMSDGTAVKGDYSQNGFGGSLEAGRTFSLNEN-----AWAQPYVRTTAF 870

Query: 568 GVNGKFSDENAHVNLG-SRQLQTRGVQ 596
 + K N +G ++ LQ G++
 Sbjct: 871 RADKKEIRLNNGMKASIGATKSLQAEAGLK 900

tr Q6G428 Hypothetical protein [BH05510] [Bartonella henselae] 874
 (Rochalimaea
 henselae)] AA
align

Score = 42.4 bits (98), Expect = 0.029
 Identities = 54/225 (24%), Positives = 90/225 (40%), Gaps = 42/225 (18%)

Query: 479 GNVKG---FGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDGTE----RFTSKG 530
 G V G + G YAT+ ++G Y DS ++Y +++++ + + G
 Sbjct: 671 GGVSGINTYSIGAYATYFD---KSGWYLDISILKYNQYQNNLKAVSTNGIAIEGNYNQWG 726

Query: 531 ITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHVNLGSR 587
 + S EAGY TK ++QP AQL++L V G K S+ +N S
 Sbjct: 727 LGTSFEAGYRF---ETTKSS---WMQPYAQQLSWLQVEGKEIKLSNEMTGDINAFTS- 776

Query: 588 QLQTRGVQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGERRVINNKTAIESQL-- 645
 L++ VG+ A +F L ++ + L N+ D IN + L
 Sbjct: 777 -LRSEVGLSAGYEFCLGGDVTSMAYITAALRENR----DSNHTTINKLHQFVTDLSG 829

Query: 646 -----GVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 G++ + L A G K Q+ QG L +++++F
 Sbjct: 830 NFGKLGIGLSSLVSKKFKLYAEAQYVKGDVKQSFQGILGVRYSF 874

tr Q83JR2 Exported serine protease SigA [sigA] [Shigella flexneri] 1285 AA
align

Score = 42.4 bits (98), Expect = 0.029
 Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQGKTAPVEGYRKGVQLGG-EVFTWQN 448
 LN + D+ D T G W R++ G S + T G K +L G ++FT
 Sbjct: 1010 LNKRGMGLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQIGVDKKHELDGLDLFT--- 1065

Query: 449 ESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGAGVYATWHQLQDKQTGAYADSWM 508
 GL + ++ N +G K GAG+YA+ +GAY D
 Sbjct: 1066 -----GLTMTYTDHAS----SNAFGKTKSVDGAGLYAS---AIFDSGAYIDLIS 1108

Query: 509 QYQRFRHRINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLT 565
 +Y + + GT+ ++S + EAGY H T+ +++PQA+L
 Sbjct: 1109 KYVHDNEYSATFAGLGTKDYSSHSLYVGAEAGYRY---HVTEDS----WIEPQAELV 1159

Query: 566 YLGNGKFSDENAHVNL---GSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALY-- 619
 Y V+GK D ++ +++ L R GV FS K+ + A + +
 Sbjct: 1160 YGAVSGKRFWDQDRGMSVTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDL 1218

Query: 620 --HNKPGVEMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGA 675

+ + + GE+R+ K I +G+ +I+ +L F + GK++
 Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNVGLNAEIRDNLRFGLEFEKSAFGKYNVDNAIN 1278
 Query: 676 LNLQWTF 682
 N +++F
 Sbjct: 1279 ANFRYSF 1285

tr Q9L8L1 Exported serine protease SigA [sigA] [Shigella flexneri 2a] 1285 AA

align

Score = 42.4 bits (98), Expect = 0.029
 Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)
 Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQGKTAGVEGYRKGVQLGG-EVFTWQN 448
 LN + D+ D T G W R++ G S + T G K +L G ++FT
 Sbjct: 1010 LNKRMGDLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQ1GVDDKHELDGLDLFT--- 1065
 Query: 449 ESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWM 508
 GL + ++ N +G K GAG+YA+ +GAY D
 Sbjct: 1066 -----GLTMTYTDASHAS-----SNAFGKTKSVGAGLYAS---AIFDSGAYIDLIS 1108
 Query: 509 QYQRFRHRINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLT 565
 +Y + + GT+ ++S + EAGY H T+ +++PQA+L
 Sbjct: 1109 KYVHHDNEYSATFAGLGTKDYSSHSLYVGAEAGYRY---HVTEDS---WIEPQAEV 1159
 Query: 566 YLGVNGKFSDSENAHVNL---GSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALY-- 619
 Y V+GK D ++ +++ L R GV FS K+ + A + +
 Sbjct: 1160 YGAVSGKRFDWQDRGMSVTMDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDL 1218
 Query: 620 --HNKPFGVEMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGA 675
 + + + GE+R+ K I +G+ +I+ +L F + GK++
 Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNVGLNAEIRDNLRFGLEFEKSAFGKYNVDNAIN 1278
 Query: 676 LNLQWTF 682
 N +++F
 Sbjct: 1279 ANFRYSF 1285

tr Q7C013 Serine protease [sigA] [Shigella flexneri] 1285 AA
align

Score = 42.4 bits (98), Expect = 0.029
 Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)
 Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQGKTAGVEGYRKGVQLGG-EVFTWQN 448
 LN + D+ D T G W R++ G S + T G K +L G ++FT
 Sbjct: 1010 LNKRMGDLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQ1GVDDKHELDGLDLFT--- 1065
 Query: 449 ESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWM 508
 GL + ++ N +G K GAG+YA+ +GAY D
 Sbjct: 1066 -----GLTMTYTDASHAS-----SNAFGKTKSVGAGLYAS---AIFDSGAYIDLIS 1108
 Query: 509 QYQRFRHRINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLT 565

+Y + + GT+ ++S + EAGY H T+ +++PQA+L
 Sbjct: 1109 KYVHHDNEYSATFAGLGTKDYSLSLYVGAEAGYRY---HVTEDS----WIEPQAEV 1159

Query: 566 YLGVNGKFDSENAHVNL---GSRQLQTRVGQAKAQFSLYKNIAIEPFAAVNALY-- 619
 Y V+GK D ++ +++ L R GV FS K+ + A + +
 Sbjct: 1160 YGAVSGKRFWDQDRGMSVTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDL 1218

Query: 620 --HNKPGVEMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGA 675
 + + + GE+R+ K I +G+ +I+ +L F + GK++
 Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNGLNAEIRDNLRFGLEFEKSAFGKYNVDNAIN 1278

Query: 676 LNLQWTF 682
 N +++F
 Sbjct: 1279 ANFRYSF 1285

tr Q8UJW1 Autotransporter protein [yapE] [Agrobacterium tumefaciens] 868
 (strain AA
 C58 / ATCC 33970) align

Score = 40.0 bits (92), Expect = 0.14
 Identities = 66/293 (22%), Positives = 113/293 (38%), Gaps = 46/293 (15%)

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQLS-IGLMGGQAEQRSTF 468
 W R ++ G +P +G G+Q G ++ + E+ GL G +
 Sbjct: 599 WARTFGQNTTEMKWDGTVSPSFDFGNLFGLQAGQDLLGRETEAGGFDRFGLFVGYSRMNGDI 658

Query: 469 HNPDT--DNLTTGNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDGE-R 525
 +NL G V G A W + + G Y D+ + F + G
 Sbjct: 659 KGQALGWNNLAVGEVDIGGTSFGAYWTHVGAQ--GWYLDALMGTWFSGDATSRAGESVN 716

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN----GKFS---DS 576
 + AS+E GY L E +T L+PQAQ+ + ++ +FS DS
 Sbjct: 717 IDGSSVAASLEGGYPIALTEDWT-----LEPQAQIIWQKLSLDDEADRFSSVAFDS 767

Query: 577 ENAHVNLLGSR---QLQTRVG-VQAKAQFSLYKNIAIEPFAAVNALYHNKPGVEMDGER 632
 +NA LG R QT G +Q + +++ + + + N P E G
 Sbjct: 768 DNAVTGRLGVRLQGNYQTDGSLIOPYLKANIWHGFSSDQMTR---FDNDPIVTETGG-- 821

Query: 633 RVINNKTAIESQLGVAVKIKSHLTLQATFNRQT---GKHHQAKQG--ALNLQW 680
 T++E G+ + +++ AT + T G+ +A +G LN++W
 Sbjct: 822 -----TSLEIGGGLVDSLTEKVSFATVDYTTNLGGERKRAIEGNIGLNIKW 868

tr Q7D396 AGR_pAT_528p [AGR_pAT_528] [Agrobacterium tumefaciens (strain] 921
 C58 / AA
 ATCC 33970) align

Score = 40.0 bits (92), Expect = 0.14
 Identities = 66/293 (22%), Positives = 113/293 (38%), Gaps = 46/293 (15%)

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVQLGGEVFTWQNESNQLS-IGLMGGQAEQRSTF 468
 W R ++ G +P +G G+Q G ++ + E+ GL G +
 Sbjct: 652 WARTFGQNTTEMKWDGTVSPSFDFGNLFGLQAGQDLLGRETEAGGFDRFGLFVGYSRMNGDI 711

Query: 469 HNPDT--DNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHINTEDGTE-R 525
 +NL G V G A W + + G Y D+ + F + G
 Sbjct: 712 KGQALGWNNLAVGEVDIGGTSFGAYWTHVGAQ--GWYLDALMGTWFSGDATSRAGESVN 769

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAOQLTYLGVN----GKFS---DS 576
 + AS+E GY L E +T L+PQAQ+ + ++ +FS DS
 Sbjct: 770 IDGSSVAASLEGGYPIALTEDWT-----LEPQAQIIWQKLSLDDEADRFSVAFDS 820

Query: 577 ENAHVNLLGSR---QLQTRVG-VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER 632
 +NA LG R QT G +Q + +++ + + + N P E G
 Sbjct: 821 DNAVTGRLGVRLQGNYQTDGLIOPYLKANIWHGFSSDQMTR----FDNDPIVTETGG-- 874

Query: 633 RVINNKTAIESQLGVAVKIKSHLTLQATFNRQT---GKHHQAKQG--ALNLQW 680
 T++E G+ + + + AT + T G+ +A +G LN++W
 Sbjct: 875 -----TSLEIGGGLVASLTEKVSVFATVDYTTNLGGERKRAIEGNIGLNIKW 921

tr Q7WK90 Autotransporter [phg] [Bordetella bronchiseptica (Alcaligenes bronchisepticus)]

align

Score = 39.7 bits (91), Expect = 0.19
 Identities = 43/213 (20%), Positives = 85/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNENQQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYAD 505
 W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D
 Sbjct: 204 WRLDTGRLYLGAYAGVSRARM----DDNDIMHGRIESRFLGTYLTYVD---NGGFYVD 254

Query: 506 SWMQYQRFRHINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
 + + R ++ + D + + T S+EAGY+ L + R +++
 Sbjct: 255 AVSKLGRIDESVFDLPLGLGDYDDDISHTTYTGSVEAGYHFKLPQ-----RWFVE 305

Query: 560 PQAQLTYLGNGKFSDENAHVNLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY 619
 PQAQ+ Y S ++ ++ G R GV+A F+L + P+ + + L+
 Sbjct: 306 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFTLAGGATLRPYVSASYLH 350

Query: 620 H-----NKPGVEMDGERRVINNKTAIE 642
 K + E+ G R + A++
 Sbjct: 351 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 383

tr Q7W8X9 Autotransporter [phg] [Bordetella parapertussis] 415 AA

align

Score = 39.7 bits (91), Expect = 0.19
 Identities = 43/213 (20%), Positives = 85/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNENQQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYAD 505
 W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D
 Sbjct: 204 WRLDTGRLYLGAYAGVSRARM----DDNDIMHGRIESRFLGTYLTYVD---NGGFYVD 254

Query: 506 SWMQYQRFRHINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
 + + R ++ + D + + T S+EAGY+ L + R +++
 Sbjct: 255 AVSKLGRIDESVFDLPLELGDYDDDISHTTYTGSVEAGYHFLRPLQ-----RWFVE 305

Query: 560 PQAQLTLYGVNGKFSDENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALY 619
 PQAQ+ Y S ++ ++ G R GV+A F+L + P+ + + L+
 Sbjct: 306 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFLAGGATLRPYVSASYLH 350

Query: 620 H-----NKPGVEMDGERRVINNKTAIE 642
 K + E+ G R + A++
 Sbjct: 351 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 383

tr Q84GK0 Secreted autotransporter protein EatA [eatA] [Escherichia coli] 1364 AA align

Score = 39.7 bits (91), Expect = 0.19
 Identities = 77/350 (22%), Positives = 136/350 (38%), Gaps = 53/350 (15%)

Query: 244 LENSLWEPRWDSNVGKLKTTNADIRFNTKSE--SLLVKEDYAGGARFRFAYDPKEAKNTA 301
 + N+LW +S + +LK ++ I + L VKE A + F + +A
 Sbjct: 928 MNNALWHSDRNSELKELKANDSQIELGVRGHFAKLRVKELIASNSVFLVHANNSQADQ-- 985

Query: 302 LIFEKNVTGTSIDIIFENPIDDLKSLDGHQIIVKNGTADKHAFRLSGKHQKGIYTLSLQQR 361
 L + G+++ I + + + +I +D++ F+ +G Q G ++ + R
 Sbjct: 986 LNVTDKLQGSNNNTILVDFFNKAANGTNVTLITAPKGSDENTFK-AGTQQIGFSNITPEIR 1044

Query: 362 PEGF-----LPKCKNAMIWRFMHNRLKPPIPYCALRLNNKNSIDFDRTLPRKGLW 411
 E +A + + + +NN N + D
 Sbjct: 1045 TENTDTATQWVLTGYQSVADARASKIATDFMDSGYKSFLTEVNNLNKRMGD----- 1095

Query: 412 LRVIDGHSNQWVQ---GKTAPVEGYRKKG---VQLGGEVFTWQNESNQLSIGLMGGQAEQR 465
 LR G + W + G + GYR VQ+G + ++E N I L G
 Sbjct: 1096 LRDSQGDAGGWARIIMNGTGSGESGYRDNYTHVQIGADR---KHELN--GIDLFTGALLTY 1150

Query: 466 STFHNPDTDNLTGKFGAGVYATWHQLQDKQTGAYADSWMQYQRF--RHRINTEDGT 523
 + N + +G K G GYVA+ ++GAY D +Y R+ +N
 Sbjct: 1151 TD--NNASSQAFSGKTKSLGGGVYASGLF---ESGAYFDLIGKYLHHDNRYTLNFASLG 1204

Query: 524 ER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPAQLTYLGVNGK 572
 ER +TS + A E GY ++E+ +++PQ +L Y V+GK
 Sbjct: 1205 ERSYTSHSLYAGAEIGYRYHMSEN-----TWVEPQMEVYGVSGK 1245

tr Q8UJX1 Autotransporter protein [bapA] [Agrobacterium tumefaciens (strain C58 / ATCC 33970)] 1035 AA align

Score = 39.3 bits (90), Expect = 0.25
 Identities = 49/199 (24%), Positives = 83/199 (41%), Gaps = 32/199 (16%)

Query: 409 GLWLRVIDGHSNQWVQGKTAPVEGYRKGV---QLGGEVFTWQNESNQL---SIGLMGGQ 461
 G+W R+ H++ + A E Y + V Q G + + ES +L + + G+
 Sbjct: 759 GVWGRIEGVHNHIEPRFSAAAAE-YDQNVFKLQAGIDGLLTETESGKLIIGGFTVHYAHGK 817

Query: 462 AEQRSTFHNPDTDNLTGKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRHINTED 521
 + RS + + + + G+G G TW+ + G Y D Q + +N+
 Sbjct: 818 TDTRSVWGDGEI-----STDGYGLGGTLWYG---ENGFYLDGQAQMTWYTGLNSLL 867

Query: 522 GTERFTSK---GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFSDS 576
 T G T S+E+G + ++ + PQAQL Y V+ F+D+
 Sbjct: 868 ARTNLTDNNNDGFGYTLSLESGTRIAIDPGWS-----VTPQAQLVYSNVDFDAFTDT 918

Query: 577 ENAHVNLLGSRQLQTRGV 595
 A V+L LQ R+GV
 Sbjct: 919 FGARVSLDRGESLQGRLGV 937

tr Q7D3A2 AGR_pAT_511p [AGR_pAT_511] [Agrobacterium tumefaciens (strain 1192
 C58 / AA
 ATCC 33970)] align

Score = 39.3 bits (90), Expect = 0.25
 Identities = 49/199 (24%), Positives = 83/199 (41%), Gaps = 32/199 (16%)

Query: 409 GLWLRVIDGHSNQWVQGKTAPVEGYRKGV---QLGGEVFTWQNESNQL---SIGLMGGQ 461
 G+W R+ H++ + A E Y + V Q G + + ES +L ++ G+
 Sbjct: 916 GVWGRIEGVHNHIEPRFSAAAAE-YDQNVFKLQAGIDGLLTESEGKLIGGFTVHYAHGK 974

Query: 462 AEQRSTFHNPDTDNLTGKVKGAGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED 521
 + RS + + + + G+G G TW+ + G Y D Q + +N+
 Sbjct: 975 TDTRSVWGDGEI-----STDGYGLGGTLTWYG---ENGFYLDGQAQMWTSGLNSLL 1024

Query: 522 GTERFTSK---GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFSDS 576
 T G T S+E+G + ++ + PQAQL Y V+ F+D+
 Sbjct: 1025 ARTNLTDNNNDGFGYTLSLESGTRIAIDPGWS-----VTPQAQLVYSNVDFDAFTDT 1075

Query: 577 ENAHVNLLGSRQLQTRGV 595
 A V+L LQ R+GV
 Sbjct: 1076 FGARVSLDRGESLQGRLGV 1094

tr Q6MTD5 Hypothetical transmembrane protein [MSC_0473] [Mycoplasma 873
 mycoides AA
 (subsp. mycoides SC)] align

Score = 38.9 bits (89), Expect = 0.32
 Identities = 45/181 (24%), Positives = 74/181 (40%), Gaps = 24/181 (13%)

Query: 27 FFSILYTSPLLAVDYVYDKTKLTNDEITRLKKLRDKTSEYWKKETYLITEDNPKVPPFPA 86
 F ++ + L ++ + KTKLT ++ +LKK +DK Y K+ +IT K
 Sbjct: 182 FNNDMLSFYLSRIENLNTKTKLTAKDLAKLKKFKDKYDFYLNKQEIQIITNKKLK----Q 236

Query: 87 LYPRTYQFENINNSKKISFYDQEYTEGYLVEGLVGFARGLGVAKRNGDTEEQIRKYFKECFNSN 146
 L Y E +N K++ + +Y E YL + +EQI K
 Sbjct: 237 LKKDQYNLELVN--KRLLKLENKY-EIYL-----NKQEIQINNNKAKLLKK 279

Query: 147 TKIRDY-STCQAEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQVIHHIE 205
 K + + C + I+ + F+ IKNS I E L + +QV+ +E
 Sbjct: 280 KKSEEIKNKCLLKLENKKQKIIINKNSFTKS-SIKNSLIKQEFLQARINKNTSSQVLETLE 338

Query: 206 N 206
 N

Sbjct: 339 N 339

sp P45386 Immunoglobulin A1 protease precursor (EC 3.4.21.72) (IGA1 1849
 IGA4_HAEIN protease)
 [iga] [Haemophilus influenzae]
align

Score = 38.5 bits (88), Expect = 0.42
 Identities = 34/142 (23%), Positives = 59/142 (40%), Gaps = 20/142 (14%)

Query: 235 QTISLDEFRL-ENSLWEPRWDSNVGKLKTTNADIRFNTKSE-----SLLVKEDYAGGA 286
 Q+I + L ENS W +SNV +L TN I N +++ + L +G

Sbjct: 852 QSIGTSQVNLKENSHTGNSNVNQLNTNGHIHLNAQNDANKVTTYNTLTVNSLSGNG 911

Query: 287 RFRFAYDPKAEAKNTALIFEKNVTG-----TSDIIFENPIDDLKSLDGH-----QIKV 334
 F + D K+ ++ K+ TG +D E ++L D ++

Sbjct: 912 SFYYWVDFTNNKSNKVVVNVKSATGNFTLQVADKTGEPNHNELTLFDASNATRNNLEVTLA 971

Query: 335 NGTADKHAFLSGKHQKGIYTL 356

NG+ D+ A++ ++ G Y L

Sbjct: 972 NGSVDRGAWKYKLRNVNGRYDL 993

tr Q9Z5R3 Phg protein (Autotransporter) [phg] [Bordetella pertussis] 418 AA

align

Score = 38.1 bits (87), Expect = 0.55
 Identities = 43/213 (20%), Positives = 84/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYAD 505
 W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D

Sbjct: 207 WRLDTGRLYLGAYAGVSRARM-----DDNDIMHRIESRFLGTYLTYVD---NGGFYVD 257

Query: 506 SWMQYQRFRHRINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
 + + R ++ + D + + T S EAGY+ L + R ++

Sbjct: 258 AVSKLGRIDESVSDPLPLGLGDYDDDISHHTYTGSAEAGYHFKLPQ-----RWFVE 308

Query: 560 PQAQLTYLGVNGKFSDSENAHVNLGSRQLQTRGVQAKAQFSLYKNIAIEPFAAVNALY 619

PQAQ+ Y S ++ ++ G R GV+A F+L + P+ + + L+

Sbjct: 309 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFTLAGGATLRPYVSASYLH 353

Query: 620 H-----NKPGVEMDGERRVINNKTIAIE 642

K + E+ G R + A++

Sbjct: 354 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 386

tr Q6KD18 Antigen 43 precursor Sap [sap] [Escherichia coli] 1042 AA
align

Score = 37.7 bits (86), Expect = 0.71
 Identities = 38/156 (24%), Positives = 65/156 (41%), Gaps = 14/156 (8%)

Query: 417 GHSNQW--VQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTD 474
 GH N V+G T G V+L G++ + L+ G+ G A S+ D D
 Sbjct: 757 GHDNNNGGIVRGATPESSGSYGFVRLEGDLLRTEVAGMSLTTGVYG--AAGHSSVDVKDDD 814

Query: 475 NLTTGNVKGFAGGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTEDGTERFTSKGITAS 534
 G V+ AG + L +G +AD Q R + +++ R +G S
 Sbjct: 815 GSRA GTVRD-DAGSLGGYLNLVHTSSGLWADIVAQGTRHSMKASSDNNDFRARGRGWQGS 873

Query: 535 IEAGYNALLAEHFTKKGNNSLRVYLQPQAQLTYLGVN 570
 +E G + ++ + L+PQ Q T+ G++
 Sbjct: 874 LETGLPFSITDN-----LMLEPQLQYTQGLS 900

tr Q8FDW4 A secreted auto transpoter toxin [sat] [Escherichia coli O6] 1299 AA

align

Score = 37.0 bits (84), Expect = 1.2
 Identities = 66/290 (22%), Positives = 114/290 (38%), Gaps = 40/290 (13%)

Query: 412 LRVIDGHSNQW--VQGKTAPVEGYRK---VQLGGEVFTWQNESNQLSIGLMGGQAEQR 465
 LR I+G S W + G + G+ VQ+G + N+ + L G
 Sbjct: 1031 LR DINGESGA WARIISGTGSAGGGFSDNYTHVQVGAD----NKHELDGLLFTGVMTY 1085

Query: 466 STFHNPDTDNLTG NVKGFAGGVYATWHQLQDKQTGAYADSWMQYQRFRHRINTED---G 522
 + H + +G K GAG+YA+ ++GAY D +Y + G
 Sbjct: 1086 TDSHAGS--DAFSGETKSVGAGLYAS---AMFESGAYIDLIGKYVHHDNEYTATFAGLG 1139

Query: 523 TERFTSKGITASIEAGYNALLAEHFTKKGNNSLRVYLQPQAQLTYLGVNGKFSDSENAHVN 582
 T ++S A E GY H T +++PQA+L Y V+GK ++ +N
 Sbjct: 1140 TRDYSSH SWYAGAEVGYRY---HVTDSA----WIEPQAEVYGA VSGKQFSWKDQGMN 1190

Query: 583 LL---GSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY---HNKPFGVEMDGERRV 634
 L L R GV FS K+ + A + + + + + GE+R+
 Sbjct: 1191 LTMKD KDFNPLIGRTGV DVGK SFS-GKDWKVTARAGLGYQFDL FAN GETV LRDAS GEKRI 1249

Query: 635 INNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGALNLQWTF 682
 K + +G+ +I+ +L F + GK++ N +++F
 Sbjct: 1250 KGEKDGRMLMN VGLNAEIRDNLRFGL EFEKSAFGKYNVDNAINANFRYSF 1299

Database: EXPASY/UniProt

Posted date: Sep 12, 2004 1:43 PM

Number of letters in database: 501,960,298

Number of sequences in database: 1,568,464

Lambda K H
 0.317 0.135 0.401

Gapped

Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 682
length of database: 501,960,298
effective HSP length: 131
effective length of query: 551
effective length of database: 296,491,514
effective search space: 163366824214
effective search space used: 163366824214
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 77 (34.3 bits)



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Entry information

Entry name	INVA_YEREN
Primary accession number	P19196
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 16, November 1990
Sequence was last modified in	Release 16, November 1990
Annotations were last modified in	Release 40, October 2001

Name and origin of the protein

Protein name	Invasin
Synonyms	None
Gene name	None
From	<u>Yersinia enterocolitica</u> [TaxID: <u>630</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=8081C / Serotype O:8;
MEDLINE=91041720;PubMed=2233250 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Young V.B.](#), [Miller V.L.](#), [Falkow S.](#), [Schoolnik G.K.](#);
 "Sequence, localization and function of the invasin protein of *Yersinia enterocolitica*.";
 Mol. Microbiol. 4:1119-1128(1990).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins.
- **SUBCELLULAR LOCATION:** Outer membrane.
- **SIMILARITY:** Belongs to the intimin/invasin family.

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RVALFGKDNL QSNPYAVTTG LIYTPIPFIT LGVDQRMGKS RQHEIQWNLQ MDYRLGESFR

310	320	330	340	350	360	
SQFSPAVVAG	TRLLAESRYN	LVERNPNIVL	EYQKQNTIKL	AFSPAVLSQL	PGQVYSVSAQ	
370	380	390	400	410	420	
IQSQSALQRI	LWNDAQWVA	GGKLIPVSAT	DYNVVLPPYK	PMAPASRTVG	KTGESEAAVN	
430	440	450	460	470	480	
TYTLSATAID	NHGNSSNPAT	LTVIVQQPQF	VITSEVTDDG	ALADGRTPIT	VKFTVTNIDS	
490	500	510	520	530	540	
TPVAEQEGVI	TTSNGALPSK	VTKKTDAQGV	ISIALTSFTV	GVSVVTLDIQ	GQQATVDVRF	
550	560	570	580	590	600	
AVLPPDVNTNS	SFNVSPSDIV	ADGSMQSI	FVPRNKNNEF	VSGITDLEFI	QSGVPVTISP	
610	620	630	640	650	660	
VTEENADNYTA	SVVGNSVGDV	DITPQVGES	LDLLQKRITL	YPVPKITGIN	VNGEQFATDK	
670	680	690	700	710	720	
GFPKTTFNKA	TFQLVMNDDV	ANNTQYDWTS	SYAASAPVDN	QGKVNIAYKT	YGSTVTVTAK	
730	740	750	760	770	780	
SKKFPSYTAT	YQFKPNLWVF	SGTMSLQSSV	EASRNCQRTD	FTALIESARA	SNGSRSPDGT	
790	800	810	820	830		
LWGEWGLSAT	YDSAEPWSGN	YWTKKTSTDF	VTMDMTTGDI	PTSAATAYPL	CAEPQ	

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Entry information

Entry name	INVA_YERPS
Primary accession number	P11922
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 12, October 1989
Sequence was last modified in	Release 12, October 1989
Annotations were last modified in	Release 45, October 2004

Name and origin of the protein

Protein name	Invasin
Synonyms	None
Gene name	None
From	<u>Yersinia pseudotuberculosis</u> [TaxID: <u>633</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

DOI=[10.1016/0092-8674\(87\)90335-7](#); MEDLINE=87301720; PubMed=3304658 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Isberg R.R.](#), [Voorhis D.L.](#), [Falkow S.](#);
 "Identification of invasin: a protein that allows enteric bacteria to penetrate cultured mammalian cells.";
[Cell](#) 50:769-778(1987).

[2] INTEGRIN-BINDING DOMAIN.

MEDLINE=90269235; PubMed=1693333 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Leong J.M.](#), [Fournier R.S.](#), [Isberg R.R.](#);
 "Identification of the integrin binding domain of the [Yersinia pseudotuberculosis](#) invasin protein.";
[EMBO J.](#) 9:1979-1989(1990).

[3] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 494-985.

DOI=[10.1126/science.286.5438.291](#); PubMed=10514372 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Hamburger Z.A.](#), [Brown M.S.](#), [Isberg R.R.](#), [Bjorkman P.J.](#);

"Crystal structure of invasin: a bacterial integrin-binding protein.";
 Science 286:291-295(1999).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins.
- **SUBCELLULAR LOCATION:** Outer surface.
- **SIMILARITY:** Belongs to the intimin/invasin family.
- **CAUTION:** It is uncertain whether Met-1, Met-17 or Met-19 is the initiator.

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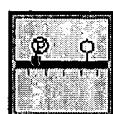
Cross-references

	M17448; AAA27633.1; -.	[EMBL] [GenBank] [DDBJ] [CoDingSequence]
EMBL	M17448; AAA27632.1; ALT_INIT.	[EMBL] [GenBank] [DDBJ] [CoDingSequence]
	M17448; AAA27634.1; ALT_INIT.	[EMBL] [GenBank] [DDBJ] [CoDingSequence]
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PIR	A29646 ; A29646.	
PDB	1CWV; X-ray; A=494-985.	[ExPASy] [RCSB] [EBI]
	IPR003344 ; Big_1.	
InterPro	IPR003535 ; Intimin.	
	IPR008964 ; Invasin_intimin.	
	Graphical view of domain structure .	
Pfam	PF02369 ; Big_1; 2.	
	Pfam graphical view of domain structure .	
PRINTS	PR01369 ; INTIMIN.	
SMART	SM00634 ; BID_1; 2.	
ProDom	[Domain structure] [List of seq. sharing at least 1 domain]	
HOBACGEN	[Family] [Alignment] [Tree]	
BLOCKS	P11922 .	
ProtoNet	P11922 .	
ProtoMap	P11922 .	
PRESAGE	P11922 .	
DIP	P11922 .	
ModBase	P11922 .	
SMR	P11922 ; C875941B24BD35EE.	
SWISS-2DPAGE	Get region on 2D PAGE .	
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.	

Keywords

3D-structure.

Features



Feature table viewer

Key

From To Length Description



Feature aligner

DOMAIN	<u>494</u>	<u>985</u>	492	Extracellular.
DOMAIN	<u>494</u>	<u>594</u>	101	D1.
DOMAIN	<u>595</u>	<u>694</u>	100	D2.
DOMAIN	<u>695</u>	<u>794</u>	100	D3.
DOMAIN	<u>795</u>	<u>985</u>	191	Integrin-binding.
DOMAIN	<u>795</u>	<u>886</u>	92	D4.
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STRAND	<u>854</u>	<u>857</u>	4
STRAND	<u>865</u>	<u>871</u>	7
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STRAND	<u>878</u>	<u>883</u>	6
STRAND	<u>887</u>	<u>891</u>	5
STRAND	<u>897</u>	<u>897</u>	1
HELIX	<u>899</u>	<u>905</u>	7
TURN	<u>906</u>	<u>906</u>	1
TURN	<u>910</u>	<u>911</u>	2
STRAND	<u>912</u>	<u>914</u>	3
STRAND	<u>916</u>	<u>916</u>	1
HELIX	<u>917</u>	<u>920</u>	4
HELIX	<u>931</u>	<u>935</u>	5
HELIX	<u>938</u>	<u>940</u>	3
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STRAND	<u>949</u>	<u>953</u>	5
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Sequence information

Length: 985 Molecular weight: 106627 CRC64: C875941B24BD35EE [This is a checksum on the sequence]

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250	260	270	280	290	300	
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LFGKDNLQRN	PYAVTAGINY	TPVPLLTGVG	DQRMGKSSKH	ETQWNLQMNY	RLGESFQSQL	
370	380	390	400	410	420	
SPSAVAGTRL	LAESRYNLVD	RNNNIVLEYQ	KQQVVKLTLS	PATISGLPGQ	VYQVNAQVQG	
430	440	450	460	470	480	
ASAVREIVWS	DAELIAAGGT	LTPLSTTQFN	LVLPPYKRTA	QVSRTDDLT	ANFYSLSALA	
490	500	510	520	530	540	
VDHQGNRSNS	FTLSVTVQQP	QLTLTAAVIG	DGAPANGKTA	ITVEFTVADF	EGKPLAGQEV	
550	560	570	580	590	600	
VITTNNGALP	NKITEKTDAN	GVARIALTNT	TDGTVVVTAE	VEGQRQSVDT	HFVKGTIAAD	
610	620	630	640	650	660	
KSTLAAVPTS	IIADGLMAST	ITLELKDTYG	DPQAGANVAF	DTTLGNMGVI	TDHNDGTYSA	
670	680	690	700	710	720	
PLTSTTLGVA	TVTVKVDGAA	FSVPSVTVNF	TADPIPDAGR	SSFTVSTPDI	LADGTMSSL	
730	740	750	760	770	780	
SFVPVDKNGH	FISGMQGLSF	TQNGVPVSIS	PITEQPDSYT	ATVVGNSVGD	VTITPQVDTL	
790	800	810	820	830	840	
ILSTLQKKIS	LFPVPTLTG	LVNGQNFATD	KGFPKTIFKN	ATFQLQMDND	VANNTQYIEWS	
850	860	870	880	890	900	
SSFTPNVSVN	DQGQVTITYQ	TYSEVAVTAK	SKKFPSSYVS	YRFYPNRWIY	DGGRSLVSSL	
910	920	930	940	950	960	
EASRQCQGSD	MSAVLESSRA	TNGTRAPDGT	LWGEW GSLTA	YSSDWQS GEY	WVKKTSTD FE	

970 980
| |
TMNMDTGALQ PGPAYLAFPL CALSI

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WEST Search History

DATE: Tuesday, September 14, 2004

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<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>				
<input type="checkbox"/>	L1	ipa\$1		29122
<input type="checkbox"/>	L2	L1 same (coli or shigella or salmonella or yersinia or rickettsia or brucella or erhlichiae or edwarsiella or campylobacter or legionella or neisseria)		479
<input type="checkbox"/>	L3	L2 and (invasin or intimin or yop)		71
<input type="checkbox"/>	L4	L3 and (lps or lipo-polysaccharide or lipopolysaccharide)		34
<input type="checkbox"/>	L5	('6245892' '20020197276' '6083683' '6680374' '6277379' '20010009957')!.PN.		10

END OF SEARCH HISTORY

Search Results - Record(s) 1 through 10 of 10 returned.

L5: Entry 1 of 10

File: PGPB

Dec 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020197276
DOCUMENT-IDENTIFIER: US 20020197276 A1

TITLE: Heterologous protection induced by immunization with invaplex vaccine
PUBLICATION-DATE: December 26, 2002

US-CL-CURRENT: 424/203.1
INT-CL: [07] A61 K 39/116

L5: Entry 2 of 10

File: PGPB

Jul 26, 2001

PGPUB-DOCUMENT-NUMBER: 20010009957
DOCUMENT-IDENTIFIER: US 20010009957 A1

TITLE: Invaplex from gram negative bacteria, method of purification and methods of use
PUBLICATION-DATE: July 26, 2001

US-CL-CURRENT: 530/395; 435/195
INT-CL: [07] C12 N 9/14, C07 K 14/24

L5: Entry 3 of 10

File: USPT

Jan 20, 2004

US-PAT-NO: 6680374
DOCUMENT-IDENTIFIER: US 6680374 B2

TITLE: Invaplex from gram negative bacteria, method of purification and methods of use

DATE-ISSUED: January 20, 2004

US-CL-CURRENT: 530/388.1; 424/130.1, 424/141.1, 424/150.1, 424/164.1, 435/329,
435/332, 435/340, 530/350, 530/388.2, 530/388.4

INT-CL: [07] C07 K 16/00, C12 P 21/08

L5: Entry 4 of 10

File: USPT

Aug 21, 2001

US-PAT-NO: 6277379
DOCUMENT-IDENTIFIER: US 6277379 B1

TITLE: Use of purified invaplex from gram negative bacteria as a vaccine

DATE-ISSUED: August 21, 2001

US-CL-CURRENT: 424/197.11; 424/193.1, 424/203.1, 424/234.1, 424/241.1, 424/249.1,
424/252.1, 424/258.1, 435/975, 530/350, 536/123.1

INT-CL: [07] A61 K 39/385

L5: Entry 5 of 10

File: USPT

Jun 12, 2001

US-PAT-NO: 6245892

DOCUMENT-IDENTIFIER: US 6245892 B1

TITLE: Invaplex from gram negative bacteria, method of purification and methods of use

DATE-ISSUED: June 12, 2001

US-CL-CURRENT: 530/350; 424/282.1, 435/7.2, 530/416

INT-CL: [07] C07 K 14/00, C07 K 1/00, G01 N 33/53, A61 K 45/00

L5: Entry 6 of 10

File: USPT

Jul 4, 2000

US-PAT-NO: 6083683

DOCUMENT-IDENTIFIER: US 6083683 A

TITLE: Methods for detecting shigella bacteria or antibodies to shigella bacteria with an immunoassay

DATE-ISSUED: July 4, 2000

US-CL-CURRENT: 435/4; 424/282.1, 424/93.4, 435/252.1, 435/29, 435/34, 435/822,
435/975

INT-CL: [07] C12 Q 1/00

L5: Entry 7 of 10

File: DWPI

Dec 3, 2002

DERWENT-ACC-NO: 2003-129359

ABSTRACTED-PUB-NO: WO 200294190A

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TITLE: Inducing in a subject a protective immune response against infection with a first invasive gram-negative bacteria by administering a composition comprising Invaplex 50 from a second heterologous invasive gram negative bacteria

INT-CL (IPC): A61 K 0/00, A61 K 39/02, A61 K 39/108, A61 K 39/112, A61 K 39/116,
A61 K 39/385, C07 K 1/00, G01 N 33/53

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04C1; B04-C02V; B04-F10A; B04-F10A3; B04-F10A5; B04-N03; B14-A01A; B14-A01A3; B14-A01A5; B14-S11B; D05-H07;

L5: Entry 8 of 10

File: DWPI

Aug 25, 2004

DERWENT-ACC-NO: 2000-292989

ABSTRACTED-PUB-NO: US 6277379B

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TITLE: New vaccine for protection against infection with gram-negative bacteria comprising Invaplex of the bacteria to elicit protective antibodies

INT-CL (IPC): A61 K 0/00, A61 K 39/02, A61 K 39/385, A61 P 31/04

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04M; B04-F10A; B04-G07; B11-C06; B14-A01A; B14-S11B; D05-H07; D05-H11;

L5: Entry 9 of 10

File: DWPI

Jan 20, 2004

DERWENT-ACC-NO: 2000-292988

ABSTRACTED-PUB-NO: US 6245892B

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TITLE: New composition comprising isolated Invaplex of gram-negative bacteria comprising at least one invasin protein associated with LPS of the gram-negative bacteria

INT-CL (IPC): A61 K 0/00, A61 K 45/00, C07 K 1/00, C07 K 14/00, C07 K 14/24, C07 K 16/00, C12 N 9/14, C12 P 21/08, G01 N 33/53

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04L; B04-B04M; B04-F01; B04-F10A; B04-N03; D05-H04; D05-H07; D05-H09; D05-H11;

L5: Entry 10 of 10

File: DWPI

Apr 7, 2003

DERWENT-ACC-NO: 1996-209840

ABSTRACTED-PUB-NO: US 5679564A

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TITLE: Prodn. of enhanced antigenic enteric bacteria for use in e.g. vaccines - uses bile acids, bile salts, oxygen, nitrogen, carbon-di:oxide and divalent cation chelant 704283 B

INT-CL (IPC): A01 N 63/00, A61 K 39/00, A61 K 39/02, A61 K 39/106, A61 K 39/108, A61 K 39/38, A61 K 45/00, A61 P 1/00, A61 P 31/04, C12 N 0/00, C12 N 1/00, C12 N 1/12, C12 N 1/20, C12 N 1/38, C12 Q 1/00, C12 Q 1/02, C12 Q 1/04, G01 N 33/53, G01 N 33/531, G01 N 33/569, C12 N 1/20, C12 R 1:19, C12 N 1/20, C12 R 1:63, C12 N 1/20, C12 R 1:42, C12 N 1/20, C12 R 1:01, C12 N 1/20, C12 R 1:19, C12 N 1/20, C12 R 1:63, C12 N 1/20, C12 R 1:42, C12 N 1/20, C12 R 1:01

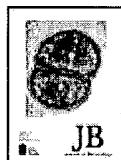
Derwent-CL (DC): B04, C07, D16, S03

CPI Codes: B04-F10A; C04-F10A; B04-G01; C04-G01; B10-B01B; C10-B01B; B11-C07A; C11-C07A; B12-K04A; C12-K04A; B14-S11B; C14-S11B; D05-H04; D05-H07; D05-H09;

EPI Codes: S03-E14H4;

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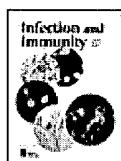
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Determination of the InvE Binding Site Required for Expression of IpaB of the *Shigella sonnei* Virulence Plasmid: Involvement of a ParB BoxA-Like Sequence

J. Bacteriol., September 1, 2003; 185(17): 5158 - 5165.

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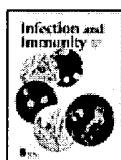
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A. T. Harrington, P. D. Hearn, W. L. Picking, J. R. Barker, A. Wessel, and W. D. Picking

Structural Characterization of the N Terminus of IpaC from *Shigella flexneri*

Infect. Immun., March 1, 2003; 71(3): 1255 - 1264.

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B. Foultier, P. Troisfontaines, D. Vertommen, M.-N. Marenne, M. Rider, C. Parsot, and G. R. Cornelis

Identification of Substrates and Chaperone from the *Yersinia enterocolitica* 1B Ysa Type III Secretion System

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S. M. Faruque, R. Khan, M. Kamruzzaman, S. Yamasaki, Q. S. Ahmad, T. Azim, G. B. Nair, Y. Takeda, and D. A. Sack

Isolation of *Shigella dysenteriae* Type 1 and *S. flexneri* Strains from Surface Waters in Bangladesh: Comparative Molecular Analysis of Environmental *Shigella* Isolates versus Clinical Strains

Appl. Environ. Microbiol., August 1, 2002; 68(8): 3908 - 3913.

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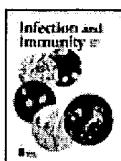
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Gut, December 1, 1998; 43(6): 752 - 758.

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Environmental Regulation of *Salmonella typhi* Invasion-Defective Mutants

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